

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	2731.5	99.3	514	6	ABP72346	Calcineur
2	2524	91.8	487	2	Aaw02336	Calcineur
3	2524	91.8	487	3	AAB14901	Partial p
4	2392.5	87.0	524	8	ADJ53606	Human PPP
5	2382	86.6	515	7	ADC99097	Human KPP
6	2370	86.2	525	7	ADB79777	Rat calci
7	2100	76.4	400	2	Aaw02537	Calcineur
8	2057.5	74.8	511	2	AAW57436	Human cal
9	2057.5	74.8	521	4	AAg67636	Amino aci
10	2057.5	74.8	521	4	AAg67457	Amino aci
11	2057.5	74.8	521	8	ADP43224	Human PPP
12	2057.5	74.8	567	8	ADR66342	Human pro
13	2057.5	74.8	567	8	ADR66684	Human pro
14	2054.5	74.7	456	5	ABB09697	Amino aci
15	2054.5	74.7	511	8	ADP43228	Rat PPP3C
16	2054.5	74.7	521	5	ABB09696	Amino aci
17	2054.5	74.7	521	8	ADF43226	Mouse PFP
18	2054.5	74.7	521	8	ADN11631	Calcineur
19	1992.5	72.5	375	2	Aaw02544	Calcineur
20	1980.5	72.0	511	8	ADK71833	Human kin
21	1980.5	72.0	511	8	ABW83040	Human dia
22	1980.5	72.0	521	8	ABW84824	Human dia
23	1912	69.5	570	4	ABB64692	Drosophil
24	1903	69.2	584	4	ABB64677	Drosophil
25	1887.5	68.6	354	2	Aaw02545	Calcineur

Db	342	LPNFMDVFTWSLPFVGEKVTETMLVNVLSICSDDELMTGEDQDPVGSAAARKELIIRNKIR	40
Qy	430	AIGKMARVPSVLRRSESESVLTLLKGLTPGTMLPSGVLAGGRQTLOSQNDVNMQLAVPQMDWG	489
Db	402	AIGKMARVPSVLRRSESESVLTLLKGLTPGTMLPSGVLAGGRQTLOSQNDVNMQLAVPQMDWG	461
Qy	490	THSFANSHNNAACREFLLFFSSCLSS	515
Db	462	TTSHFANSHNNAACRELLLLFFSSCLSS	487
RESULT 3			
ID	AAB14901		
AC	AAB14901 standard; protein; 487 AA.		
CC	AAB14901;		
XX	08-JAN-2001 (first entry)		
XX	Partial protein encoded by murine T cell library cDNA clone 11.1.		
DE	Mouse; calcineurin-binding peptide; A-kinase anchor protein; AKAP;		
XX	AKAP 79; immunostimulant; interleukin 2 expression modulation;		
KW	graft rejection; transplantation; T cell-mediated disorder.		
KW			
OS	Mus sp.		
XX			
US	US6107104-A.		
PN	XX		
XX	22-AUG-2000.		
PD	XX		
XX	27-SEP-1996; 96US-00721458.		
PF	XX		
XX	23-NOV-1994; 94US-00344227.		
PR	15-MAR-1995; 95US-00404731.		
PR	17-JUL-1995; 95US-00503226.		
PR			
PA	(ICOS-) ICOS CORP.		
XX			
XX	Lockerbie RO, Gallatin WM, Lai Y, Howard ML;		
PI	WPI; 2000-578541/54.		
XX	N-PSDB; AAA94251.		
DR	XX		
DR	XX		
XX	Novel calcineurin deletion mutant having calcineurin polypeptide sequence		
PT	and binding A-kinase anchor proteins, for treating graft rejection		
PT	following organ transplantation and T cell-mediated disorders.		
XX	XX		
PS	Claim 1; Col 53-56; 53pp; English.		
XX	XX		
CC	The present sequence is encoded by clone 11.1 of a murine T cell cDNA		
CC	library which was subjected to a yeast dihybrid assay using A-kinase		
CC	anchor protein 79 (AKAP 79) as the bait. The sequence was found to be		
CC	closely homologous to the human calmodulin dependent protein phosphatase,		
CC	calcineurin, thus demonstrating that calcineurin binds to AKAP 79.		
CC	Calcineurin is involved in many intracellular signalling pathways and		
CC	participates in regulation of IL-2 expression following T cell		
CC	stimulation in T cells. By binding both CAMP-dependent protein kinase		
CC	(pKA) and calcineurin, AKAP 79 co-localises a kinase and a phosphatase		
CC	that may regulate flux through a specific signalling pathway. Calcineurin		
CC	-binding peptides derived from AKAP 79 may be used to inhibit calcineurin		
CC	activity in a cell. The peptides are useful for treating graft rejection		
CC	following organ transplantation and for treating T cell-mediated		
CC	disorders. Calcineurin deletion mutants which bind AKAP 79 are useful for		
CC	defining an AKAP 79 binding site, for stimulating the immune response,		
CC	stimulating activated T cells for selected clonal expansion, or for		
CC	enhancing T cell responses to experimental stimuli for evaluation of		
CC	early events in T cell biology and activation of the immune response		
XX	XX		
SQ	Sequence 487 AA;		
SQ	SQ		

Query Match 91.8%; Score 2524; DB 3; Length 487;
Best Local Similarity 94.9%; Pred. No. 1.8e-227;

Matches	480; Conservative	2; Mismatches	4; Indels	20; Gaps	3;																																																						
Qy	11	PPPPPPPPPPGADRVVKA	PPPPPT	HLRTS	EEVFDLDGIPRVDLK	KNHLVK	EGRV	DE	EA	70																																																	
Db	1	PPPPPPPPPLGADRVVKA	PPPPPT	HLRTS	EEVFDMDGIPRVDLK	KNHLVK	EGRV	DE	EA	60																																																	
Qy	71	LRINSGAAILRREK	TMIE	VEAPIT	VC	DIHG	QFPDL	MKL	FEV	GSGSPANTRYL	PLGDYD	130																																															
Db	61	LRINSGAAILRREK	TMIE	VEAPIT	VC	DIHG	QFPDL	MKL	FEV	GSGSPANTRYL	PLGDYD	120																																															
Qy	131	RGVFS	TEHVL	GTED	IS	INPHNN	INE	CVL	WL	VL	KILY	PS	TL	F	LL	LL	RG	NH	EC	R	HL	TE	Y	TF	190																																		
Db	121	RGVFS	T	E	H	V	L	G	T	E	D	I	S	I	N	P	H	N	N	I	N	E	C	V	L	W	L	K	I	L	Y	P	S	T	L	F	L	L	R	G	N	H	E	C	R	H	L	T	E	Y	T	F	161						
Qy	191	KQECKI	KY	S	E	R	V	Y	E	A	C	M	E	A	F	D	S	L	P	L	A	A	L	N	Q	P	L	C	V	H	G	L	S	P	E	I	H	T	L	D	D	I	R	R	L	D	R	F	K	E	P	P	250						
Db	162	KQECKI	KY	S	E	R	V	Y	E	A	C	M	E	A	F	D	S	L	P	L	A	A	L	N	Q	P	L	C	V	H	G	L	S	P	E	I	H	T	L	D	D	I	R	R	L	D	R	F	K	E	P	P	221						
Qy	251	AFQPM	CD	L	W	S	D	S	E	D	F	G	N	E	K	S	Q	E	H	F	S	H	N	T	V	R	G	C	S	Y	F	N	Y	P	A	V	C	E	P	L	O	N	N	L	L	S	I	T	R	A	H	E	310						
Db	222	AFQPM	CD	L	W	S	D	S	E	D	F	G	N	E	K	S	Q	E	H	F	S	H	N	T	V	R	G	C	S	Y	F	N	Y	P	A	V	C	E	P	L	O	N	N	L	L	S	I	T	R	A	H	E	281						
Qy	311	AQ	D	A	G	Y	M	R	K	S	O	T	T	G	P	S	L	I	T	F	S	A	P	N	Y	L	D	V	N	N	K	A	A	V	L	K	Y	E	N	N	V	N	T	I	R	O	F	N	C	S	P	H	P	Y	370				
Db	282	AQ	D	A	G	Y	M	R	K	S	O	T	T	G	P	S	L	I	T	F	S	A	P	N	Y	L	D	V	N	N	K	A	A	V	L	K	Y	E	N	N	V	N	T	I	R	O	F	N	C	S	P	H	P	Y	341				
Qy	371	LP	N	F	M	D	V	T	W	S	L	P	F	V	G	E	K	V	T	E	M	L	V	N	Y	L	S	I	C	S	D	D	E	L	M	T	E	G	E	D	F	D	-	G	S	A	A	R	K	E	I	R	N	K	I	R	429		
Db	342	LP	N	F	M	D	V	T	W	S	L	P	F	V	G	E	K	V	T	E	M	L	V	N	Y	L	S	I	C	S	D	D	E	L	M	T	E	G	E	D	F	D	V	G	S	A	A	R	K	E	I	R	N	K	I	R	401		
Qy	430	A	I	G	K	M	A	R	V	F	S	L	R	E	E	S	E	S	V	L	T	K	G	L	T	P	T	G	M	L	P	S	G	V	T	A	G	G	R	T	L	O	S	G	N	D	V	M	Q	L	A	V	P	Q	M	D	W	G	489
Db	402	A	I	G	K	M	A	R	V	F	S	L	R	E	E	S	E	S	V	L	T	K	G	L	T	P	T	G	M	L	P	S	G	V	T	A	G	G	R	T	L	O	S	G	N	D	V	M	Q	L	A	V	P	Q	M	D	W	G	461
Qy	490	T	P	H	S	P	A	N	N	H	N	A	C	R	E	F	L	L	P	F	S	S	C	L	S	51																																	

or Alzheimer's disease.

Example 13; SEQ ID NO 4; 91pp; English.

The invention relates to an antisense oligonucleotide targeted to a nucleic acid encoding the human PPP3CB polypeptide and inhibits expression of the PPP3CB polypeptide. The antisense oligonucleotide comprises at least one modified internucleoside linkage, i.e. a phosphorothioate linkage, at least one modified sugar moiety, preferably a 2'-O-methoxyethyl sugar moiety, or at least one modified nucleobase comprising a 5-methylcytosine. The antisense oligonucleotides are useful for inhibiting expression of the PPP3CB polypeptide and in preparation of a composition for treating autoimmune disorders or Alzheimer's disease. This sequence represents the human PPP3CB polypeptide of the invention.

Sequence 524 AA;

Query Match 87.0%; Score 2392.5; DB 8; Length 524;
 Best Local Similarity 96.0%; Pred. No. 4.3e-215;
 Matches 455; Conservative 0; Mismatches 0; Indels 19; Gaps 2;

QY 1 MAAPEPARAAPP PPPPPPPGADRVVKA VPPPTHLRTSEVFDLGIPRDVVLKNHLV 60
 DB 1 MAAPEPARAAPP PPPPPPPGADRVVKA VPPPTHLRTSEVFDLGIPRDVVLKNHLV 60
 QY 61 KEGRVDEEIALRIINEGAAILRREKTMIEVEAPITVCGDIHGQFFDLMKLFEVGGSPANT 120
 DB 61 KEGRVDEEIALRIINEGAAILRREKTMIEVEAPITVCGDIHGQFFDLMKLFEVGGSPANT 120
 QY 121 RYFLFGDYVDRGVFSIEHVLGTEDISINPHNNINECVLYLWVLKILYPSLTFLLRGNHE 180
 DB 121 RYFLFGDYVDRGVFSI-----ECVLYLWVLKILYPSLTFL--LLRGNHE 161
 QY 181 CRHLYEYFTFKQECKIKYSERVYACMEAFDLSPLAALLNQOFLCVHGGLSPEIHTLDDI 240
 DB 162 CRHLYEYFTFKQECKIKYSERVYACMEAFDLSPLAALLNQOFLCVHGGLSPEIHTLDDI 221
 QY 241 RRLDRFKEPPAFGPMCDLLKSDPSEDFGNEKSQHFHNTVCGSYFYNNYPAVCEFLQNN 300
 DB 222 RRLDRFKEPPAFGPMCDLLKSDPSEDFGNEKSQHFHNTVCGSYFYNNYPAVCEFLQNN 281
 QY 301 NLLSIIRAHAQDAGYRMYSKQTTGFPSSLITIFSAFNLDVYNNKAAVLKYENNVNIR 360
 DB 282 NLLSIIRAHAQDAGYRMYSKQTTGFPSSLITIFSAFNLDVYNNKAAVLKYENNVNIR 341
 QY 361 QFNCSPPHYLWLPNMDVFTWSLPVGSKVTEMLVNVLSICSDDELMTEGSDQFDGSAAR 420
 DB 342 QFNCSPPHYLWLPNMDVFTWSLPVGSKVTEMLVNVLSICSDDELMTEGSDQFDGSAAR 401
 QY 421 KEIIRNKIRAIKGMARVSVLRESESVLTILKGLTPTGMLPSGLVAGGRTLOS 474
 DB 402 KEIIRNKIRAIKGMARVSVLRESESVLTILKGLTPTGMLPSGLVAGGRTLOS 455

RESULT 5
 ADC99097
 ID ADC99097 standard; protein; 515 AA.

XX AC ADC99097;
 XX DT 01-JAN-2004 (first entry)
 XX DE Human KPP protein - SEQ ID 50.

XX anti-HIV; anti-allergic; anti-inflammatory; antianemic; antiparkinsonian;
 KW nootropic; anticonvulsant; antiarteriosclerotic; antiasthmatic;
 KW immunosuppressive; antithyroid; cytostatic; hepatotropic; dermatological;
 KW antidiabetic; nephrotropic; antigout; thyromimetic; neuroprotective;
 KW osteopathic; antiarthritic; antiparasitic; antihelminthic; antipeptic;
 KW uropathic; ophthalmological; antirheumatic; haemostatic; antibacterial;
 KW virucide; protozoacide; fungicide; kinase; phosphatase; KPP;
 KW cell proliferative disorder; atherosclerosis; cirrhosis; hepatitis;
 KW cancer; developmental; mental retardation; neurological;

Alzheimer's disease; Parkinson's; autoimmune; inflammatory; Crohn's;
 diabetes mellitus; viral; bacterial; fungal; parasitic; protozoan;
 helminthic infection; transgenic; gene therapy; human; enzyme.

Homo sapiens.

WO2003033680-A2.

24-APR-2003.

17-OCT-2002; 2002WO-US033723.

19-OCT-2001; 2001US-0345474P.

02-NOV-2001; 2001US-0343910P.

13-NOV-2001; 2001US-0333098P.

16-NOV-2001; 2001US-0332424P.

30-NOV-2001; 2001US-0334288P.

(INCY-) INCYTE GENOMICS INC.

Bandnan O, Baughn MR, Becha SD, Borowsky ML, Duggan BM;
 Emerling R, Forsythe IJ, Gandhi AR, Gorvad AE, Griffin JA;
 Gururajan R, Hafalia AJA, Khan FA, Lal PG, Lee EA, Lee SY;
 Lindquist EA, Lu DAM, Lu Y, Marguis JP, Nguyen DB, Arvizu CS;
 Ramkumar J, Recipon SA, Richardson TW, Swarnakar A, Tang YT;
 Thornton MB, Tran UK, Chawla NK, Warren BA, Yang J, Yao MG, Yue H;
 Zebbarjadian Y;

WPI; 2003-403214/38.
 N-PSDB; ADC99149.

New human kinases and phosphatases and polynucleotides, useful for
 diagnosing, treating or preventing autoimmune or inflammatory disorders
 (e.g. AIDS, allergy or anemia), multiple sclerosis, osteoarthritis,
 cancer or hepatitis.

Claim 1; SEQ ID NO 50; 424pp; English.

The invention relates to a novel isolated polypeptide which is a human
 kinase and phosphatase (KPP). The KPP polypeptides, polynucleotides,
 agonists and antagonists are useful for diagnosing, treating or
 preventing cell proliferative disorders such as atherosclerosis,
 cirrhosis, hepatitis and cancer, developmental disorders, e.g. mental
 retardation, neurological disorders including Alzheimer's disease and
 Parkinson's disease, autoimmune and inflammatory disorders such as
 Crohn's disease and diabetes mellitus and finally, viral, bacterial,
 fungal, parasitic, protozoan or helminthic infections. Furthermore, the
 polynucleotides encoding KPP may be useful for creating transgenic
 animals to model human disease, as well as during gene therapy
 procedures. The current sequence is that of the human KPP protein of the
 invention.

Sequence 515 AA;

Query Match 86.6%; Score 2382; DB 7; Length 515;
 Best Local Similarity 95.8%; Pred. No. 4.1e-214;
 Matches 455; Conservative 0; Mismatches 0; Indels 20; Gaps 3;

QY 1 MAAPEPARAAPP PPPPPPPGADRVVKA VPPPTHLRTSEVFDLGIPRDVVLKNHLV 60
 DB 1 MAAPEPARAAPP PPPPPPPGADRVVKA VPPPTHLRTSEVFDLGIPRDVVLKNHLV 60
 QY 61 KEGRVDEEIALRIINEGAAILRREKTMIEVEAPITVCGDIHGQFFDLMKLFEVGGSPANT 120
 DB 61 KEGRVDEEIALRIINEGAAILRREKTMIEVEAPITVCGDIHGQFFDLMKLFEVGGSPANT 120
 QY 121 RYFLFGDYVDRGVFSIEHVLGTEDISINPHNNINECVLYLWVLKILYPSLTFLLRGNHE 180
 DB 121 RYFLFGDYVDRGVFSI-----ECVLYLWVLKILYPSLTFL--LLRGNHE 161
 QY 181 CRHLYEYFTFKQECKIKYSERVYACMEAFDLSPLAALLNQOFLCVHGGLSPEIHTLDDI 240
 DB 162 CRHLYEYFTFKQECKIKYSERVYACMEAFDLSPLAALLNQOFLCVHGGLSPEIHTLDDI 221

QY 241 RRLDRFKPEPPAFGPMCDLLWSDPSEDFGNEKSEQEHFSHTNVRGCSYFYNYPAVCBFLQNN 300
 |||||
 DB 222 RRLDRFKPEPPAFGPMCDLLWSDPSEDFGNEKSEQEHFSHTNVRGCSYFYNYPAVCBFLQNN 281
 |||||
 QY 301 NLLSIIRAHEAQAQAGYMYRKSQTTGFPFSLITIFSAFNLDVYNNKAAVLYKYENNVMNIR 360
 |||||
 DB 282 NLLSIIRAHEAQAQAGYMYRKSQTTGFPFSLITIFSAFNLDVYNNKAAVLYKYENNVMNIR 341
 |||||
 QY 361 QFNCSPPHPVWLPNFMDFVFTWSLPPFVGEKVTEMLVNVLSICSDDELMTEGDEQDFD-GSAAA 419
 |||||
 DB 342 QFNCSPPHPVWLPNFMDFVFTWSLPPFVGEKVTEMLVNVLSICSDDELMTEGDEQDFD-GSAAA 401
 |||||
 QY 420 RKEIIRNKIRAIGKMARVSVLRESESVLTILKGLTPTGMLPSGVLAGGRTQLQS 474
 |||||
 DB 402 RKEIIRNKIRAIGKMARVSVLRESESVLTILKGLTPTGMLPSGVLAGGRTQLQS 456
 |||||
 RESULT 6
 ADB79777
 ID ADB79777 standard; protein; 525 AA.
 XX
 AC ADB79777;
 XX
 DT 04-DEC-2003 (first entry)
 XX
 DE Rat calcineurin, A subunit, beta isoform, SEQ ID 17.
 XX
 KW Analgesic; pain; streptozocin-induced diabetes; rat.
 XX
 OS Rattus norvegicus.
 XX
 PN EP1279744-A2.
 XX
 PD 29-JAN-2003.
 XX
 PF 26-JUL-2002; 2002EP-00255249.
 XX
 PR 27-JUL-2001; 2001GB-00018354.
 PR 07-FEB-2002; 2002GB-00002910.
 XX
 PA (WARN) WARNER LAMBERT CO.
 XX
 PI Brooksbank RA, Dixon AK, Lee K, Pinnock RD;
 XX
 DR WPI; 2003-345407/38.
 DR N-PSDB; ADB79778.
 XX
 PT Use of isolated gene sequences and encoded polypeptides that are
 PT upregulated in the spinal cord in response to streptozocin-induced
 PT diabetes for screening compounds for the treatment of pain, or for
 PT diagnosing pain.
 XX
 PS Claim 1; Page 66-67; 334pp; English.
 XX
 CC The present invention relates to nucleotide sequences which are useful in
 CC the screening of compounds for the treatment of pain, or for the
 CC diagnosis of pain. The nucleotide sequences are up-regulated in the
 CC spinal cord in response to streptozocin-induced diabetes. The present
 CC sequence was used to illustrate the invention.
 XX
 SQ Sequence 525 AA;
 Query Match 86.2%; Score 2370; DB 7; Length 525;
 Best Local Similarity 95.4%; Pred. No. 5.6e-213;
 Matches 453; Conservative 1; Mismatches 1; Indels 20; Gaps 3;
 QY 1 MAAPEPARAAPPPPPPPPPGADRVKAVPPPPPHRLTSEVFDLGDIGIPRVVLKNHLV 60
 |||||
 DB 1 MAAPEPARAAPPPPPPPPPGADRVKAVPPPPPHRLTSEVFDLGDIGIPRVVLKNHLV 60
 |||||
 QY 61 KEGRVDEBIAURIIINEGAAILRREKTMIEVAPITVCGDIHQGFDFMLMKLFEVGGSPANT 120
 |||||

DB 61 KEGRVDEBIAURIIINEGAAILRREKTMIEVAPITVCGDIHQGFDFMLMKLFEVGGSPANT 120
 |||||
 QY 121 RYFLGDYVDVDRGYFSIEHVLGTEDISINPHNNINECVLYLWVLYKILYESTLFLLLRGNHE 180
 |||||
 DB 121 RYFLGDYVDVDRGYFSI-----ECVLYLWVLYKILYESTLFL-LLRGNHE 161
 |||||
 QY 181 CRHLYTEYFTFKQECKIKYSERVYEAQMEAFDLSPLAALLNQOFLCVHGGLSPEIHTLDDI 240
 |||||
 DB 162 CRHLYTEYFTFKQECKIKYSERVYEAQMEAFDLSPLAALLNQOFLCVHGGLSPEIHTLDDI 221
 |||||
 QY 241 RRLDRFKPEPPAFGPMCDLLWSDPSEDFGNEKSEQEHFSHTNVRGCSYFYNYPAVCBFLQNN 300
 |||||
 DB 222 RRLDRFKPEPPAFGPMCDLLWSDPSEDFGNEKSEQEHFSHTNVRGCSYFYNYPAVCBFLQNN 281
 |||||
 QY 301 NLLSIIRAHEAQAQAGYMYRKSQTTGFPFSLITIFSAFNLDVYNNKAAVLYKYENNVMNIR 360
 |||||
 DB 282 NLLSIIRAHEAQAQAGYMYRKSQTTGFPFSLITIFSAFNLDVYNNKAAVLYKYENNVMNIR 341
 |||||
 QY 361 QFNCSPPHPVWLPNFMDFVFTWSLPPFVGEKVTEMLVNVLSICSDDELMTEGDEQDFD-GSAAA 419
 |||||
 DB 342 QFNCSPPHPVWLPNFMDFVFTWSLPPFVGEKVTEMLVNVLSICSDDELMTEGDEQDFD-GSAAA 401
 |||||
 QY 420 RKEIIRNKIRAIGKMARVSVLRESESVLTILKGLTPTGMLPSGVLAGGRTQLQS 474
 |||||
 DB 402 RKEIIRNKIRAIGKMARVSVLRESESVLTILKGLTPTGMLPSGVLAGGRTQLQS 456
 |||||
 RESULT 7
 AAW02537
 ID AAW02537 standard; protein; 400 AA.
 XX
 AC AAW02537;
 XX
 DT 13-JAN-1997 (first entry)
 XX
 DE Calcineurin deletion mutant 1-400.
 XX
 KW Autoimmune disease; pACT59; pACT74; pACT36; pACT60; murine; T-cell; PKA;
 KW mouse; A-kinase anchoring protein 79; cAMP-dependent protein kinase;
 KW postsynaptic density; AKAP79; human forebrain; transcriptional activator;
 KW interleukin 2; T-cell activation; calcineurin; T-cell clonal expansion;
 KW calcium/calmodulin dependent protein phosphatase; T-cell response;
 KW autoimmune related disease; therapy; immune response.
 XX
 OS Synthetic.
 XX
 PN WO9616172-A2.
 XX
 PD 30-MAY-1996.
 XX
 PF 22-NOV-1995; 95WO-US016039.
 XX
 PR 23-NOV-1994; 94US-00344227.
 PR 15-MAR-1995; 95US-00404731.
 PR 17-JUL-1995; 95US-00503226.
 XX
 PA (ICOS-) ICOS CORP.
 PA (OREG-) STATE OF OREGON.
 PA (UYOR-) UNIV OREGON HEALTH SCI.
 PA (UYOR-) UNIV OREGON HEALTH SCI.
 XX
 PI Lockertbie RO, Coghlan VM, Howard ML, Gallatin WM, Scott JD;
 XX
 DR WPI; 1996-268608/27.
 XX
 PT New modulators of anchoring protein function - used to develop prods. for
 PT use in the treatment of auto-immune-related conditions.
 XX
 PS Claim 16; Page 7; 74pp; English.
 XX
 CC AAW02537-W02556 represent calcineurin (see AAW02536 for full length
 CC sequence) deletion mutants. Calcineurin is a calcium/calmodulin dependent
 CC protein phosphatase associated with T-cell activation. Calcineurin is

bound by A-kinase anchoring protein 79 (AKAP79). AKAP79 is responsible for anchoring CAMP-dependent protein kinase (PKA) to specific intracellular sites. AKAP79 is predominantly present in postsynaptic densities in the human forebrain. The pathways that involve AKAP79 are important in many cell types and have been implicated in many cell functions, including the transcriptional activation of the interleukin 2 gene that is important in T-cell activation. By binding both PKA and calcineurin, AKAP79 co-localises a kinase and a phosphatase which may regulate flux through a specific signalling pathway. These sequences can be used in a method for identifying a compound that inhibits binding between an anchor protein (such as AKAP79) and a binding partner. AKAP79 binding sequences can be used to develop products for use in the treatment of autoimmune related conditions. The AKAP79 binding proteins can be used in methods for stimulating an immune response, and for stimulating activated T-cells for selected clonal expansion. The proteins can also be used in a method for enhancing T-cell responses to experimental stimuli for evaluation of early events in T-cell biology and activation of the immune response

SQ Sequence 400 AA;

Query Match 76.4%; Score 2100; DB 2; Length 400;
Best Local Similarity 94.7%; Pred. No. 8.1e-189;
Matches 397; Conservative 1; Mismatches 1; Indels 20; Gaps 3;

QY 11 PPPPPPPPPGADRVKAVPPPPHRLTSEVFDLGI PRVDVLKNHLVKEGRVDEEIA 70
DB 1 PPPPPPPPPGADRVKAVPPPPHRLTSEVFDMDGIPRVDVLKNHLVKEGRVDEEIA 60

QY 71 LRIINEGAAILRREKTMIEVEAPITVCGDIHQGFQFDLMKLFVGGSPANTRYLFLGDYVD 130
DB 61 LRIINEGAAILRREKTMIEVEAPITVCGDIHQGFQFDLMKLFVGGSPANTRYLFLGDYVD 120

QY 131 RGYFSIEHVLGTEDISINPHNNINECVLYLWLVKILYPSLTLFLLRGNHECHRLTEYFTF 190
DB 121 RGYFSI-----ECVLYLWLVKILYPSLTLF-LLRGNHECHRLTEYFTF 161

QY 191 KOECKIKYSERYVEACMEAFDSLPLAALLNQOFLCVHGGLSPEIHTLDDIRLDRFKPEPP 250
DB 162 KOECKIKYSERYVEACMEAFDSLPLAALLNQOFLCVHGGLSPEIHTLDDIRLDRFKPEPP 221

QY 251 AFGPMDLLWSDPSDFGNEKSQEHFSHNTVRGCSFYFNYPVAVCFEFLQNNLLSIIRAHE 310
DB 222 AFGPMDLLWSDPSDFGNEKSQEHFSHNTVRGCSFYFNYPVAVCFEFLQNNLLSIIRAHE 281

QY 311 AQDAGYRMYSKQTTGPPSLITIFSAPNYLDVYNNKAAVLKYENNVMNIRQNCSPHPYWP 370
DB 282 AQDAGYRMYSKQTTGPPSLITIFSAPNYLDVYNNKAAVLKYENNVMNIRQNCSPHPYWP 341

QY 371 LPNFMVDVFTWSLPPFVGEKVTMLVNLVSLCSDDDELMTGEDQFD-GSAAARKEIIRNKI 428
DB 342 LPNFMVDVFTWSLPPFVGEKVTMLVNLVSLCSDDDELMTGEDQFDVGSAAARKEIIRNKI 400

RESULT 8
AAR57436
ID AAR57436 standard; protein; 511 AA.
XX AAR57436;
AC AAR57436;
XX 18-MAY-1995 (first entry)
XX Human calcineurin A isoform protein.
XX Calcineurin A isoform protein; antibody; diagnosis; identification;
KW nervous system; tumour.
XX Homo sapiens.
XX JP06181778-A.
XX 05-JUL-1994.
XX PD
XX

PF 16-DEC-1992; 92JP-00335935.
XX 16-DEC-1992; 92JP-00335935.
XX (TAKE) TAKEDA CHEM IND LTD.
XX WPI; 1994-251696/31.
DR N-PSDB; AAQ67085.
XX

Human calcineurin A alpha isoform protein DNA - useful in study of nerve physiology and biochemistry.

PS Claim 3; Page 9; 14pp; Japanese.

XX The DNA sequence (See AAQ67085) and the encoded protein are useful in research on nerve physiology and biochemistry. The protein may be used to raise antibodies which are useful as diagnostic agents for the identification of nervous system tumours

SQ Sequence 511 AA;

Query Match 74.8%; Score 2057.5; DB 2; Length 511;
Best Local Similarity 83.6%; Pred. No. 1.1e-183;
Matches 387; Conservative 34; Mismatches 21; Indels 21; Gaps 4;

QY 13 PPPPPPPPPGADRVKAVPPPPHRLTSEVFDLGI PRVDVLKNHLVKEGRVDEEIALR 72
DB 4 PKAIDPKLSTDRVKAAPPPPSHRLTAKVFNDDGKPRVDIILKAHLMKSGRUESEVALR 63

QY 73 IINEGAAILRREKTMIEVEAPITVCGDIHQGFQFDLMKLFVGGSPANTRYLFLGDYVDRG 132
DB 64 IITEGASILRQENKLLDIDAPVTVCGDIHQGFQFDLMKLFVGGSPANTRYLFLGDYVDRG 123

QY 133 YFSIEHVLGTEDISINPHNNINECVLYLWLVKILYPSLTLFLLRGNHECHRLTEYFTFKQ 192
DB 124 YFSI-----ECVLYLWLVKILYPSLTLF-LLRGNHECHRLTEYFTFKQ 164

QY 193 ECKIKYSERYVEACMEAFDSLPLAALLNQOFLCVHGGLSPEIHTLDDIRLDRFKPEPPAF 252
DB 165 ECKIKYSERYVDACMDAFDCLPLAALMNQOFLCVHGGLSPEIHTLDDIRLDRFKPEPPAY 224

QY 253 GPMCDLLWSDPSDFGNEKSQEHFSHNTVRGCSFYFNYPVAVCFEFLQNNLLSIIRAHEAQ 312
DB 225 GPMCDLLWSDPSDFGNEKTEQEHFTHTVRGCSFYFYSPVAVCFEFLQNNLLSIIRAHEAQ 284

QY 313 DAGYRMYSKQTTGPPSLITIFSAPNYLDVYNNKAAVLKYENNVMNIRQNCSPHPYWP 372
DB 285 DAGYRMYSKQTTGPPSLITIFSAPNYLDVYNNKAAVLKYENNVMNIRQNCSPHPYWP 344

QY 373 NFMVDVFTWSLPPFVGEKVTMLVNLVSLCSDDDELMTGEDQFDG-SAAARKEIIRNKIRAI 431
DB 345 NFMVDVFTWSLPPFVGEKVTMLVNLVSLCSDDDELMTGEDQFDG-SAAARKEIIRNKIRAI 403

QY 432 GKMARVSVLRESESVLTLKGLTPTGMLPSGVLGGKQTLQS 474
DB 404 GKMARVSVLRESESVLTLKGLTPTGMLPSGVLGGKQTLQS 446

RESULT 9
AAG67636
ID AAG67636 standard; protein; 521 AA.
XX AAG67636;
AC AAG67636;
XX 26-NOV-2001 (first entry)
XX Amino acid sequence of a human protein.
XX Human; protein kinase; protein phosphatase; signal transduction.
XX Homo sapiens.
XX WO200109316-A1.
XX

```
XX PD 08-FEB-2001.
XX PF
XX PR 28-JUL-2000; 2000WO-JP005061.
XX PR 29-JUL-1999; 99JP-00248036.
XX PR 18-OCT-1999; 99US-0159590P.
XX PR 11-JAN-2000; 2000JP-00118776.
XX PR 17-FEB-2000; 2000US-0183322P.
XX PR 02-MAY-2000; 2000JP-00183767.
XX PR 09-JUN-2000; 2000JP-00241899.
XX PA (HELI-) HELIX RES INST.
XX PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
XX PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T, Funahashi S;
XX PI Senoo C, Nezu J;
XX WPI; 2001-570286/64.
XX DR
XX PT New genes encoding proteins with protein kinase/protein phosphatase
XX PT activity, useful in the diagnosis and treatment of diseases.
XX PS Example 4; Page 201-205; 233pp; Japanese.
XX CC The specification describes human protein kinase/protein phosphatases. It
XX CC is expected that the protein kinase/protein phosphatase gene participates
XX CC in signal transduction in cells. The protein kinase/protein phosphatase
XX CC polypeptides and polynucleotides are useful for developing diagnostics
XX CC and treatment agents for human and animal diseases. The protein
XX CC kinase/protein phosphatase polypeptides are useful as target molecules in
XX CC designing novel drugs. The protein kinase/protein phosphatase
XX CC polynucleotides are useful as a source of probes and primers, which may
XX CC be used to isolate homologous sequences. The present sequence represents
XX CC a human protein, which is used in the course of the invention
XX SQ
XX SQ Sequence 521 AA;
XX Query Match 74.8%; Score 2057.5; DB 4; Length 521;
XX Best Local Similarity 83.6%; Pred. No. 1.2e-183;
XX Matches 387; Conservative 34; Mismatches 21; Indels 21; Gaps 4;
XX QY 13 PPPPPPPGADRVVKA VPPFPPTHLRTSEEVFDLDGIPRDVILKNHLVKEGRVDEIALR 72
XX Db 4 PKAIDPKLSTTDVVKA VPPFPSPHRLTAKEVFDNDGKPRVDILKAHLMEGRLEESVALR 63
XX QY 73 IINEGAAILRRKTMIEVEAPITVCGDIHGQFDFMLMKLFEVGGSPANTRYILFLGDYVDRG 132
XX Db 64 IITEGASILROEKLLDIDAPVTVCGDTHGQFDFMLMKLFEVGGSPANTRYILFLGDYVDRG 123
XX QY 133 YFSIEHVLGTEDISINPHNINECVLYLWVILKILYPSLTLFLLLRGNHRCRLHTEYFTFKQ 192
XX Db 124 YFSI-----ECVLYLWALKILYPKTLF-LLRGNHRCRLHTEYFTFKQ 164
XX QY 193 ECKIKYSERVYBACMEAFDLSPLAALLNQQLFCVHGGLSPEIHTLDDIRRLDRFKEPPAF 252
XX Db 165 ECKIKYSERVYDADCFDLPLAALMQQLFCVHGGLSPEIHTLDDIRKLDKRPKEPPAY 224
XX QY 253 GPMCDLLWSDPSDEGNGKESQHFHSHNTVRGCSYFYNTYPAVCEFLQNNLLSITRAHRAQ 312
XX Db 225 GPMCDILWSDPLEDFGNEKTSQHFHTNTVRGCSYFYSPYPAVCEFLQNNLLSILRAHRAQ 284
XX QY 313 DAGYRMYRKSQTTGPPSLITTFSAADYLDVYNNKAALVLYNNVNIQFNCSPHPYWL 372
XX Db 285 DAGYRMYRKSQTTGPPSLITTFSAADYLDVYNNKAALVLYNNVNIQFNCSPHPYWL 344
XX QY 373 NPMDFVFTWSLPVGEKVTMLVNVLSICSDDELMTEGEDQFDG-SAAARKEIIRNKIRAI 431
XX Db 345 NPMDFVFTWSLPVGEKVTMLVNVLSICSDDELMTEGEDQFDG-EDGFDGATAAARKEVIRNKIRAI 403
XX QY 432 GGMARVFSVLRSESVLTAKGLTPTGMLPGSVLAGGRQTLOS 474
XX Db 404 GGMARVFSVLRSESVLTAKGLTPTGMLPGSVLAGGRQTLOS 446
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RESULT 10
AAG67457
XX ID AAG67457 standard; protein; 521 AA.
XX AC AAG67457;
XX DT 26-NOV-2001 (first entry)
XX DE Amino acid sequence of a human polypeptide.
XX KW Human; protein kinase; protein phosphatase; signal transduction;
XX KW intracellular signalling pathway.
XX OS Homo sapiens.
XX PN WO200109345-A1.
XX PD 08-FEB-2001.
XX PF 28-JUL-2000; 2000WO-JP005060.
XX PR 29-JUL-1999; 99JP-00248036.
XX PR 18-OCT-1999; 99US-0159590P.
XX PR 11-JAN-2000; 2000JP-00118776.
XX PR 17-FEB-2000; 2000US-0183322P.
XX PR 02-MAY-2000; 2000JP-00183767.
XX PA (HELI-) HELIX RES INST.
XX PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
XX PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T, Funahashi S;
XX PI Senoo C, Nezu J;
XX WPI; 2001-564736/63.
XX DR
XX PT New genes encoding protein kinase and protein phosphatase, useful for
XX PT identifying modulators which can be used to treat human or animal
XX PT disorders associated with the expression or function of these enzymes.
XX PS Example 4; Page 301-305; 336pp; Japanese.
XX CC The specification describes human protein kinase/protein phosphatases.
XX CC The polypeptides are expected to participate in signal transduction in
XX CC cells. The kinase phosphatases are connected with intracellular
XX CC signalling pathways. Antisense oligonucleotides and compounds identified
XX CC by screening (agonists or antagonists) can be used to treat human or
XX CC animal disorders associated with the expression or function of the
XX CC protein. In addition, the polypeptides may be used as target molecules
XX CC for drug development. The present sequence represents a polypeptide, used
XX CC in the course of the invention
XX SQ
XX SQ Sequence 521 AA;
XX Query Match 74.8%; Score 2057.5; DB 4; Length 521;
XX Best Local Similarity 83.6%; Pred. No. 1.2e-183;
XX Matches 387; Conservative 34; Mismatches 21; Indels 21; Gaps 4;
XX QY 13 PPPPPPPGADRVVKA VPPFPPTHLRTSEEVFDLDGIPRDVILKNHLVKEGRVDEIALR 72
XX Db 4 PKAIDPKLSTTDVVKA VPPFPSPHRLTAKEVFDNDGKPRVDILKAHLMEGRLEESVALR 63
XX QY 73 IINEGAAILRRKTMIEVEAPITVCGDIHGQFDFMLMKLFEVGGSPANTRYILFLGDYVDRG 132
XX Db 64 IITEGASILROEKLLDIDAPVTVCGDTHGQFDFMLMKLFEVGGSPANTRYILFLGDYVDRG 123
XX QY 133 YFSIEHVLGTEDISINPHNINECVLYLWVILKILYPSLTLFLLLRGNHRCRLHTEYFTFKQ 192
XX Db 124 YFSI-----ECVLYLWALKILYPKTLF-LLRGNHRCRLHTEYFTFKQ 164
XX QY 193 ECKIKYSERVYBACMEAFDLSPLAALLNQQLFCVHGGLSPEIHTLDDIRRLDRFKEPPAF 252
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CC cancer by differential expression analysis, using DNA microarrays,
 CC between normal and tumorous tissues, with (over)expression being detected
 CC by quantitative PCR. Analysis of prostatic cancer samples showed that
 CC CD24 was upregulated in many of them. Sections of tissue, isolated from
 CC prostatic cancer patients, or subjects at risk, were incubated
 CC sequentially with anti-human CD4 murine monoclonal antibodies;
 CC biotinylated second antibody; streptavidin-conjugated horseradish
 CC peroxidase and then diaminobenzidine as colour former (brown). The
 CC samples were counterstained with hemalum (blue). Malignant cells stained
 CC strongly but non-malignant cells only weakly. In 15 of 63 samples of
 CC adenocarcinoma, membrane and cytoplasmic staining was very strong, and
 CC lymph node metastases were also stained. ADR65805-ADR6954 represent the
 CC polynucleotide and polypeptide sequences used in the method of the
 CC invention.

XX SQ Sequence 567 AA;

Query Match 74.8%; Score 2057.5; DB 8; Length 567;
 Best Local Similarity 83.6%; Pred. No. 1.3e-183;
 Matches 387; Conservative 34; Mismatches 21; Indels 21; Gaps 4;
 QY 13 P P P P P P P P G A D R V V K A V P P P P T H R L T S E V F D L G I P R V D V L K N H L V K E G R V D E E I A L R 72
 DB 50 P K A I D P K L S T T D R V V K A V P P P P S H R L T A K E V F D N G K P R V D I L K A H L M K E G R L E S V A L R 109
 QY 73 I I N E G A I L R E K T M I E V A P I T V C G D I H G Q F F D L M K L F E V G G S P A N T R Y L F L G D Y Y D R G 132
 DB 110 I I T E G A S I L R Q E K N L D I D A P V T V C G D I H G Q F F D L M K L F E V G G S P A N T R Y L F L G D Y Y D R G 169
 QY 133 Y F S I E H V L G T E D I S I N P H N N I E C V L Y L W L V L K I L Y P S T L F L L R G N H E C H R L T E Y F T F K Q 192
 DB 170 Y F S I ----- E C V L Y L W A L K I L Y P K T L F - L L R G N H E C H R L T E Y F T F K Q 210
 QY 193 E C K I K Y S E R V Y E A C M E A F D S L P L A A L N Q O F L C V H G G L S P E I H T L D D I R K L D R F K E P P A F 252
 DB 211 E C K I K Y S E R V Y D A C M D A F D C L P L A A L M N Q O F L C V H G G L S P E I N T L D D I R K L D R F K E P P A Y 270
 QY 253 G P M C D I L W S D P S E D F G N E K S Q E H F S H N T V R G C S Y F Y N P A V C F L Q N N L L S I L R A H E A Q 312
 DB 271 G P M C D I L W S D P L E D F G N E K T Q E H T H N T V R G C S Y F Y S P A V C F L Q N N L L S I L R A H E A Q 330
 QY 313 D A G Y R M Y R K S Q T T G F P S L I T I F S A P N Y L D V Y N N K A A V L K Y E N N V M N I R Q F N C S P H P Y W L P 372
 DB 331 D A G Y R M Y R K S Q T T G F P S L I T I F S A P N Y L D V Y N N K A A V L K Y E N N V M N I R Q F N C S P H P Y W L P 390
 QY 373 N F M D V F T W S L P F V G E K V T E M L V N V L S I C S D D E L M T E G D Q F D G - S A A A R K E I I R N K I R A I 431
 DB 391 N F M D V F T W S L P F V G E K V T E M L V N V L N I C S D D E L G S E - E D G F D G A T A A A R K E V I R N K I R A I 449
 QY 432 G K M A R V F S V L R E E S E S V L T L K G L T P T G M L P S G V L A G G R Q T L O S 474
 DB 450 G K M A R V F S V L R E E S E S V L T L K G L T P T G M L P S G V L S G G K Q T L O S 492

RESULT 14

ABB09697
 ID ABB09697 standard; protein; 456 AA.

XX AC ABB09697;

XX DT 11-JUN-2002 (first entry)

XX DE Amino acid sequence of human calcineurin short isoform.

XX KW Human; calcineurin; neuronal stress; excitotoxicity;
 KW neurodegenerative disease; Alzheimer's disease; Parkinson's disease;
 KW Huntington's disease; multiple sclerosis; cerebral ischaemia;
 KW amyotrophic lateral sclerosis.

XX OS Homo sapiens.

XX PN WO20020872-A2.

XX XX

PD 03-JAN-2002.
 XX 28-JUN-2001; 2001WO-FR002058.
 XX 29-JUN-2000; 2000FR-00008407.
 PR (EXON-) EXONHIT THERAPEUTICS SA.

XX Alet Ikhlef A, Resink A, Schweighoffer F;
 WIPI; 2002-130890/17.
 DR N-PSDB; ABL41922.

XX Use of nucleic acid encoding calcineurin for diagnosis and detection of
 PT neuronal stress.

XX Claim 17; Page 31-32; 32pp; French.

XX The present sequence represents the short isoform of human calcineurin.
 CC Calcineurin is present in two isoforms, a long isoform and a short
 CC isoform. In the short isoform, nucleotides 1341-1741 (corresponding to
 CC amino acids 447-524) of the long isoform are deleted. Calcineurin
 CC contains an auto-inhibitor domain, which is deleted in the short isoform.
 CC Sequences derived from the mRNA of the catalytic subunit of calcineurin
 CC are used for diagnosis and detection of neuronal stress, particularly
 CC excitotoxicity. Compounds that inhibit or reduce expression or activity
 CC of the catalytic subunit of calcineurin are used for treatment of
 CC neurodegenerative diseases. Calcineurin is used for diagnosis and
 CC detection of Alzheimer's, Parkinson's or Huntington's diseases, multiple
 CC sclerosis and cerebral ischaemia. Compounds that inhibit or reduce
 CC expression or activity of the catalytic subunit of calcineurin are useful
 CC for treating these diseases and amyotrophic lateral sclerosis

XX SQ Sequence 456 AA;

Query Match 74.7%; Score 2054.5; DB 5; Length 456;
 Best Local Similarity 83.4%; Pred. No. 1.8e-183;
 Matches 386; Conservative 35; Mismatches 21; Indels 21; Gaps 4;
 QY 13 P P P P P P P P G A D R V V K A V P P P P T H R L T S E V F D L G I P R V D V L K N H L V K E G R V D E E I A L R 72
 DB 4 P K A I D P K L S T T D R V V K A V P P P S H R L T A K E V F D N G K P R V D I L K A H L M K E G R L E S V A L R 63
 QY 73 I I N E G A I L R E K T M I E V A P I T V C G D I H G Q F F D L M K L F E V G G S P A N T R Y L F L G D Y Y D R G 132
 DB 64 I I T E G A S I L R Q E K N L D I D A P V T V C G D I H G Q F F D L M K L F E V G G S P A N T R Y L F L G D Y Y D R G 123
 QY 133 Y F S I E H V L G T E D I S I N P H N N I E C V L Y L W L V L K I L Y P S T L F L L R G N H E C H R L T E Y F T F K Q 192
 DB 124 Y F S I ----- E C V L Y L W A L K I L Y P K T L F - L L R G N H E C H R L T E Y F T F K Q 164
 QY 193 E C K I K Y S E R V Y E A C M E A F D S L P L A A L N Q O F L C V H G G L S P E I H T L D D I R K L D R F K E P P A F 252
 DB 165 E C K I K Y S E R V Y D A C M D A F D C L P L A A L M N Q O F L C V H G G L S P E I N T L D D I R K L D R F K E P P A Y 224
 QY 253 G P M C D I L W S D P S E D F G N E K S Q E H F S H N T V R G C S Y F Y N P A V C F L Q N N L L S I L R A H E A Q 312
 DB 225 G P M C D I L W S D P L E D F G N E K T Q E H T H N T V R G C S Y F Y S P A V C F L Q N N L L S I L R A H E A Q 284
 QY 313 D A G Y R M Y R K S Q T T G F P S L I T I F S A P N Y L D V Y N N K A A V L K Y E N N V M N I R Q F N C S P H P Y W L P 372
 DB 285 D A G Y R M Y R K S Q T T G F P S L I T I F S A P N Y L D V Y N N K A A V L K Y E N N V M N I R Q F N C S P H P Y W L P 344
 QY 373 N F M D V F T W S L P F V G E K V T E M L V N V L S I C S D D E L M T E G D Q F D G - S A A A R K E I I R N K I R A I 431
 DB 345 N F M D V F T W S L P F V G E K V T E M L V N V L N I C S D D E L G S E - E D G F D G A T A A A R K E V I R N K I R A I 403
 QY 432 G K M A R V F S V L R E E S E S V L T L K G L T P T G M L P S G V L A G G R Q T L O S 474
 DB 404 G K M A R V F S V L R E E S E S V L T L K G L T P T G M L P S G V L S G G K Q T L O S 446

RESULT 15

ADP43228
ID ADP43228 standard; protein; 511 AA.
XX
AC ADP43228;
XX
DT 26-FEB-2004 (first entry)
XX
DE Rat PPP3CA amino acid sequence SEQ ID NO:20.
XX
XX diabetic; pre-diabetic; Type 2 diabetes; diabetes; insulin resistance;
KW metabolic disease; antidiabetic; rat.
XX
OS Rattus sp.
XX
FN WO2003101284-A2.
XX
PD 11-DEC-2003;
XX
PP 04-JUN-2003; 2003WO-US017941.
XX
PR 04-JUN-2002; 2002US-0385996P.
PR 04-JUN-2002; 2002US-0386113P.
PR 06-JUN-2002; 2002US-0386812P.
PR 06-JUN-2002; 2002US-0386935P.
PR 06-JUN-2002; 2002US-0386956P.
PR 06-JUN-2002; 2002US-0386958P.
PR 06-JUN-2002; 2002US-0387038P.
XX
PA (META-) METABOLEX INC.
XX
PI Bernard A, Lavan B, Moodie S, Waters S, Wong C;
XX
DR WPI; 2004-071055/07.
DR N-PSDB; ADP43227.
XX
PT Identifying an agent for treating diabetes and insulin resistance
PT comprising selecting an agent that modulates the expression or activity
PT of a polypeptide or that binds to the polypeptide.
XX
PS Disclosure; SEQ ID NO 20; 95pp; English.
XX
SS
CC The present invention describes a method for identifying an agent for
CC treating a diabetic or pre-diabetic individual comprising: (a) contacting
CC an agent to a mixture comprising a polypeptide encoded by a nucleic acid
CC that hybridises under stringent conditions to a nucleic acid encoding a
CC sequence comprising the 373 amino acids (ADP43210), 288 amino acids
CC (ADP43216), 1036 amino acids (ADP43220), 521 amino acids (ADP43224), 913
CC amino acids (ADP43230), 868 amino acids (ADP43234), 185 amino acids
CC (ADP43236), or 167 amino acids (ADP43240); and (b) selecting an agent
CC that modulates the expression or activity of the polypeptide or that
CC binds to the polypeptide. Also described: (1) treating a diabetic or pre-
CC diabetic animal; (2) introducing an expression cassette into a cell; (3)
CC diagnosing an individual who has Type 2 diabetes or is pre-diabetic; (4)
CC an isolated nucleic acid (ADP43233) encoding a polypeptide comprising 869
CC amino acids (ADP43234); (5) an expression vector comprising the nucleic
CC acid of (4); and (6) a host cell comprising the expression vector of (5).
CC The method is useful for identifying an agent for treating a diabetic or
CC pre-diabetic individual. The agent is useful for diagnosing or treating
CC diabetes. The polypeptides and modulators of the polypeptides are useful
CC for diagnosing or treating diabetes, pre-diabetes (including insulin
CC resistant individuals) and related metabolic diseases. The present
CC sequence is used in the exemplification of the present invention.
XX
SQ Sequence 511 AA;

Query Match 74.7%; Score 2054.5; DB 8; Length 511;
Best Local Similarity 83.4%; Pred. No. 2.2e-183;
Matches 386; Conservative 35; Mismatches 21; Indels 21; Gaps 4;
13 PPPPPPPPGADRVVKA VPPPPHRLTSEEVFDLDGIPRVDLVNLVKGSRVDEIALR 72
4 PKAIDPKLSTTDVVVKA VPPPPHRLTAKEVFDNDGRPRVDILKAHLKMGRLSEVALR 63

Search completed: February 26, 2005, 14:24:49
Job time : 178.927 secs

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Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	2392.5	87.0	524	1	P2BB_HUMAN	P16299 homo sapien
2	2389.5	86.9	524	2	Q8HZM9	Q8HZM9 oryctolagus
3	2382	86.6	515	2	Q8N3W4	Q8N3W4 homo sapien
4	2382	86.6	525	2	Q8N1F0	Q8N1F0 homo sapien
5	2370	86.2	525	1	P2BB_MOUSE	P48453 mus musculus
6	2370	86.2	525	1	P2BB_RAT	P20651 rattus norv
7	2060.5	74.9	504	2	Q7T1F5	Q7T1F5 gallus gall
8	2057.5	74.8	511	2	Q8TAW9	Q8TAW9 homo sapien
9	2057.5	74.8	511	2	Q8HZN0	Q8HZN0 oryctolagus
10	2057.5	74.8	521	1	P2BA_HUMAN	Q08209 homo sapien
11	2056.5	74.8	521	1	P2BA_BOVIN	P48452 bos taurus
12	2054.5	74.7	511	2	Q9WU77	Q9WU77 rattus norv
13	2054.5	74.7	521	1	P2BA_MOUSE	P63328 mus musculus
14	2054.5	74.7	521	1	P2BA_RAT	P63329 rattus norv
15	2052.5	74.6	511	2	Q9SMZ3	Q9SMZ3 sus scrofa
16	2051.5	74.6	511	2	Q6ARXB0	Q6ARXB0 xenopus lae
17	2047.5	74.5	508	2	Q9DEF7	Q9DEF7 xenopus lae
18	2047.5	74.5	518	2	Q801N4	Q801N4 xenopus lae
19	2066	72.9	507	2	Q61R94	Q61R94 xenopus lae
20	1998.5	72.7	518	2	O57438	O57438 xenopus lae
21	1985	72.2	502	1	P2BC_HUMAN	P48454 homo sapien
22	1985	72.2	502	2	Q9H4M5	Q9H4M5 homo sapien
23	1985	72.2	512	2	Q9BS56	Q9BS56 homo sapien
24	1924	70.0	538	2	Q80XK0	Q80XK0 mus musculus
25	1919.5	69.8	513	1	P2BC_MOUSE	P48455 mus musculus
26	1918.5	69.8	506	2	O6AYJ0	O6AYJ0 rattus norv
27	1912.5	69.5	524	2	Q7PKK6	Q7PKK6 anopheles g
28	1912	69.5	486	2	Q9NKM8	Q9NKM8 patinopecte
29	1912	69.5	570	2	Q9VXF2	Q9VXF2 drosophila
30	1904.5	69.3	485	2	Q9D5R5	Q9D5R5 mus musculus
31	1903	69.2	478	2	Q2T573	Q2T573 drosophila


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QY 421 KEIIRNKIRAIKGMARVSVLREESVLTGLTPTGMLPSGVLAGGRQTLOS 474
Db 402 KEIIRNKIRAIKGMARVSVLREESVLTGLTPTGMLPSGVLAGGRQTLOS 455

RESULT 3
ID Q8N3W4 PRELIMINARY; PRT; 515 AA.
AC Q8N3W4;
DT 01-OCT-2002 (TremBLrel. 22, Created)
DT 01-OCT-2002 (TremBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TremBLrel. 26, Last annotation update)
DE Protein phosphatase 3 catalytic subunit beta3 (EC 3.1.3.16).
GN Name=PPP3CB;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Cohen P.T.W.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
phosphate.
CC -1- SIMILARITY: Belongs to the PPP phosphatase family.
DR EMBL; AJ48506; CAD32694.1; -.
DR HSSP; Q08209; IAU1.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0004721; F:phosphoprotein phosphatase activity; IEA.
DR InterPro; IPR004843; M-pesterase.
DR InterPro; IPR006186; T_ptase_apah.
DR Pfam; PF00149; Metallophos; 1.
DR PRINTS; PR00114; STPHPTASE.
DR ProDom; PD000252; T_ptase_apah; 1.
DR SMART; SM00156; PP2Ac; 1.
DR PROSITE; PS00125; SER_THR_PHOSPHATASE; UNKNOWN_1.
KW Hydrolase; Iron.
SQ SEQUENCE 515 AA; 58081 MW; A6762D9468A09B51 CRC64;

Query Match 86.6%; Score 2382; DB 2; Length 515;
Best Local Similarity 95.8%; Pred. No. 2.7e-172;
Matches 455; Conservative 0; Mismatches 0; Indels 20; Gaps 3;

QY 1 MAAPPARAAPP PPPPPGADRVVKAAPP PPHRLTSTSEVFDLGI PRVDVLKNHLV 60
Db 1 MAAPPARAAPP PPPPPGADRVVKAAPP PPHRLTSTSEVFDLGI PRVDVLKNHLV 60

QY 61 KEGRVDEIARIINEGAAILREKTMLEVEAPITVCGDIHQCFDMLKLFVGGSPANT 120
Db 61 KEGRVDEIARIINEGAAILREKTMLEVEAPITVCGDIHQCFDMLKLFVGGSPANT 120

QY 121 RYFLGDIVDRGYFSI EHVLTGDIINPHNNINECVLYLWVLTLYPSTLFLLRGNHE 180
Db 121 RYFLGDIVDRGYFSI EHVLTGDIINPHNNINECVLYLWVLTLYPSTLFLLRGNHE 161

QY 181 CRHLYTEYTFKQCKIKYSERYVEACMEAFDSLPALALNQOFLCVHGLGLSPEIHTLDDI 240
Db 162 CRHLYTEYTFKQCKIKYSERYVEACMEAFDSLPALALNQOFLCVHGLGLSPEIHTLDDI 221

QY 241 RLRLRFKPPAFGPMCDLLWSDPFCGNEKSHQEHFNTVRGCSFYFNPVAVCEFLQNN 300
Db 222 RLRLRFKPPAFGPMCDLLWSDPFCGNEKSHQEHFNTVRGCSFYFNPVAVCEFLQNN 281

QY 301 NLLSIIRAHEAQDAGYRMYRSQTTGFPSPITIFSAPNYLDVYNNKAAVLKYENNVNMR 360

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Query Match 86.6%; Score 2382; DB 2; Length 525;
 Best Local Similarity 95.8%; Pred. No. 2.7e-172;

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Matches 455; Conservative 0; Mismatches 0; Indels 20; Gaps 3;
QY 1 MAAPEPARAAAPPPPPPPPPGADRVKAVFPFPHRLTSEVFDLGIIPVDVVKHLY 60
Db 1 MAAPEPARAAAPPPPPPPPPGADRVKAVFPFPHRLTSEVFDLGIIPVDVVKHLY 60
QY 61 KEGRVDEIALRIINEGAAILRREKTMIEVEAPITVCGDIGHQGFDMKLFVEVGGSPANT 120
Db 61 KEGRVDEIALRIINEGAAILRREKTMIEVEAPITVCGDIGHQGFDMKLFVEVGGSPANT 120
QY 121 RYFLGVDVDRGYFSIEHVLGTEDISINPHNNINECVLYLWVLKILYPTSLFLLLRGHNE 180
Db 121 RYFLGVDVDRGYFSI-----ECVLYLWVLKILYPTSLFL-LLRGHNE 161
QY 181 CRHLTEVFTFKQECKIKYSERVYACMEAFDSLPALALNNQOFLCVHGGLSPEHTITDDI 240
Db 162 CRHLTEVFTFKQECKIKYSERVYACMEAFDSLPALALNNQOFLCVHGGLSPEHTITDDI 221
QY 241 RRLDRFKEPPAFGPMCDLLWSDPSEDGNEKSQEHFSHTVGRGSYFYNYPAVCEFLQNN 300
Db 222 RRLDRFKEPPAFGPMCDLLWSDPSEDGNEKSQEHFSHTVGRGSYFYNYPAVCEFLQNN 281
QY 301 NLSIIRAEQAQDAGYRMYRSQTTGFPPLTIFSAFNLDVYNKKAALVKYENNVNIR 360
Db 282 NLSIIRAEQAQDAGYRMYRSQTTGFPPLTIFSAFNLDVYNKKAALVKYENNVNIR 341
QY 361 QFNCSPPHYWLPNFMVFTWSLPFVGEKVTEMLVNVLSICSDDELMTGEDEQDFD-GSAAA 419
Db 342 QFNCSPPHYWLPNFMVFTWSLPFVGEKVTEMLVNVLSICSDDELMTGEDEQDFDVGAAA 401
QY 420 RKEIIRNKIRAIKGKARVFSVLRESESVLTGKLTPTGMLPSGVLGGRTQLQS 474
Db 402 RKEIIRNKIRAIKGKARVFSVLRESESVLTGKLTPTGMLPSGVLGGRTQLQS 456
RESULT 5
P2BB MOUSE
ID P2BB MOUSE STANDARD; PRT; 525 AA.
AC P48453; Q6NZR4;
DT 01-FEB-1996 (Rel. 33, Created)
DT 25-JAN-2005 (Rel. 46, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Serine/threonine protein phosphatase 2B catalytic subunit, beta
DE isoform (EC 3.1.3.16) (Calmodulin-dependent calcineurin A subunit,
DE beta isoform) (CAM-PRP catalytic subunit).
GN Name=Ppp3cb; Synonyms=Calnb;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426038899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins B.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U.,
RA Sutterch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
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RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE OF 11-525 FROM N.A. (ISOFORM 2).
RX MEDLINE=92068200; PubMed=1659808;
RA Giri P.R., Higuchi S., Kincaid R.L.;
RT "Chromosomal mapping of the human genes for the calmodulin-dependent
RL Biochem. Biophys. Res. Commun. 181:252-258(1991).
RN [3]
RP SEQUENCE OF 320-416 FROM N.A. (ISOFORMS 1 AND 2), AND TISSUE
RP SPECIFICITY.
RX PubMed=1328240;
RA Gaestel M., Bendoric R., Hayess K., Priemer E., Engel K.;
RT "Dephosphorylation of the small heat shock protein hsp25 by
calcium/calmodulin-dependent (type 2B) protein phosphatase.";
RL J. Biol. Chem. 267:21607-21611(1992).
CC -1- FUNCTION: Calcium-dependent, calmodulin-stimulated protein
phosphatase. This subunit may have a role in the calmodulin
activation of calcineurin.
CC -1- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
phosphate.
CC -1- COFACTOR: Binds 1 iron(III) ion and 1 zinc ion per subunit (By
similarity).
CC -1- SUBUNIT: Composed of two components (A and B), the A component is
the catalytic subunit and the B component confers calcium
sensitivity.
CC -1- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
Name=2; Synonyms=2B2;
IsoId=P48453-1; Sequence=Displayed;
Name=1; Synonyms=2B1;
IsoId=P48453-2; Sequence=VSP_011856;
CC -1- TISSUE SPECIFICITY: Two isoforms in Ehrlich ascites tumor (EAT) is
demonstrated by polymerase chain reaction specific primers to the
catalytic and calmodulin-binding domain, respectively. Isoform 1
is of medium abundance in EAT cells.
CC -1- SIMILARITY: Belongs to the PPP phosphatase family. PP-2B
subfamily.
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EMBL; BC066000; AAH66000.1; -.
EMBL; M81483; AAA37411.1; -.
FIR; JT0976; JT0976.
HSP; Q08209; IAU1.
MGD; MG1:107163; Ppp3cb.
GO; GO:0004722; F:protein serine/threonine phosphatase activity; IDA.
GO; GO:0007507; P:heart development; IMP.
GO; GO:0006470; P:protein amino acid dephosphorylation; IMP.
GO; GO:0030217; P:T-cell differentiation; IMP.
InterPro; IPR004843; N-esterase.
InterPro; IPR006186; T:phosphatase_apah.
PFam; PF00149; Metallophos; 1.
PRINTS; PR00114; STPHPTASE.
ProDom; PD000252; T:phosphatase_apah; 1.
SMART; SM00156; PP2AC; 1.
PROSITE; PS00125; SER_THR_PHOSPHATASE; 1.
Alternative splicing; Calmodulin-binding; Hydrolase; Iron;
Metal-binding; Multigene family; Protein phosphatase; Zinc.
DOMAIN 1 310 Catalytic.
DOMAIN 11 20 Poly-Pro.
DOMAIN 256 262 Calcineurin B binding-site 1 (Potential).
DOMAIN 305 310 Calcineurin B binding-site 2 (Potential).
DOMAIN 401 423 Calmodulin-binding (Potential).
DOMAIN 474 496 Inhibitory domain.
METAL 99 99 Iron (By similarity).
METAL 101 101 Iron (By similarity).
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FT METAL 127 Iron and zinc (By similarity).
 FT METAL 159 Zinc (By similarity).
 FT ACT SITE 160 Proton donor (By similarity).
 FT METAL 208 Zinc (By similarity).
 FT METAL 230 Zinc (By similarity).
 FT VARSP LIC 387 MTEGSDQDVGSAARKEII -> GSEEDGDFGATAAARKE
 VI (in isoform 1).
 FT 481 /FTID=VSP_011856.
 FT CONFLICT 481 E -> G (in Ref. 2).
 FT CONFLICT 523 SA -> TP (in Ref. 2).
 SQ SEQUENCE 525 AA; 59173 MW; 5E73BA3100BE2337 CRC64;

Query Match 86.2%; Score 2370; DB 1; Length 525;
 Best Local Similarity 95.4%; Pred. No. 2.2e-171;
 Matches 453; Conservative 1; Mismatches 1; Indels 20; Gaps 3;

QY 1 MAAPPARAAAPPPPPPPPPGADRVKAVKAVPPPPHRLTSEVFDLGI PRVDVLKHLV 60
 DB 1 MAAPPARAAAPPPPPPPPPGADRVKAVKAVPPPPHRLTSEVFDMDGIPRVVDLKHLV 60

QY 61 KEGRVDEIALRIINEGAAILRREKTMIEVEAPITVCGDIHQGFDMKLFVGGSPANT 120
 DB 61 KEGRVDEIALRIINEGAAILRREKTMIEVEAPITVCGDIHQGFDMKLFVGGSPANT 120

QY 121 RYFLGDYVDRGYFSIEHVLGTEDISINPHNNIECVLYLWLVKILYPSITLFLLRGNHE 180
 DB 121 RYFLGDYVDRGYFSI-----ECVLYLWLVKILYPSITLFL-LLRGNHE 161

QY 181 CRHLYTEYTFKQECKIKYSERYVEACMEAPDSLPALALNQOFLCVHGLSPETHLDDI 240
 DB 162 CRHLYTEYTFKQECKIKYSERYVEACMEAPDSLPALALNQOFLCVHGLSPETHLDDI 221

QY 241 RRLDRFKEPPAFGPMCDLLWSDPSDFGNEKSEQHFSHTVGRGCSFYFNPVAVCEFLQNN 300
 DB 282 NLLSIIRAHAQDAGYRMYRSQTTGFPPLITIFSAPNYLDVYNNKAAVLKYENNVNMR 341

QY 361 QFNCSPHYPLNFMNDVFTWSLPFVGEKVTMLVNLVSLICSDDELMTGEDEQDFD-GSAAA 419
 DB 342 QFNCSPHYPLNFMNDVFTWSLPFVGEKVTMLVNLVSLICSDDELMTGEDEQDFDVGSA 401

QY 420 RKEIIRNKIRAIKGMARVSVLRESESVTLKGLTPTGMLPSGVLAGGRTQLQS 474
 DB 402 RKEIIRNKIRAIKGMARVSVLRESESVTLKGLTPTGMLPSGVLAGGRTQLQS 456

RESULT 6
 P2BB RAT
 ID P2BB RAT STANDARD; PRT; 525 AA.

AC P20651.
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Serine/threonine protein phosphatase 2B catalytic subunit, beta
 DE isoform (BC 3.1.3.16) (Calmodulin-dependent calcineurin A subunit,
 DE beta isoform) (CAM-PRP catalytic subunit).
 GN Name=Pp3cb;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 ON NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90121248; PubMed=2558657;
 RA Kuno T., Takeda T., Hirai M., Ito A., Mukai H., Tanaka C.;
 RT "Evidence for a second isoform of the catalytic subunit of calmodulin-
 dependent protein phosphatase (calcineurin A).";
 RL Biochem. Biophys. Res. Commun. 165:1352-1358(1989).
 CC -!- FUNCTION: Calcium-dependent, calmodulin-stimulated protein
 phosphatase. This subunit may have a role in the calmodulin

activation of calcineurin.
 -!- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein + phosphate.
 -!- COFACTOR: Binds 1 iron(III) ion and 1 zinc ion per subunit (By similarity).
 -!- SUBUNIT: Composed of two components (A and B), the A component is the catalytic subunit and the B component confers calcium sensitivity.
 -!- SIMILARITY: Belongs to the PPP phosphatase family. PP-2B subfamily.

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EMBL; M31809; AAA40848.1; -;
 EMBL; D90036; BAA14084.1; -;
 PIR; A33794; A33794.
 HSSP; Q08209; 1AUI.
 RGD; 3383; Pp3cb.
 InterPro; IPR004943; M-pesterase.
 InterPro; IPR006186; T_phtase_apah.
 Pfam; PF00149; Metallophos; 1.
 PRINTS; PR00114; STPHPTASE.
 ProDom; PD000252; T_phtase_1.
 SMART; SM00156; Pp2AC; 1.
 PROSITE; PS00125; SSR_THR_PHOSPHATASE; 1.
 Calmodulin-binding; Hydrolase; Iron; Metal-binding; Multigene family;
 Protein phosphatase; Zinc.
 DOMAIN 1 310 Catalytic.
 FT DOMAIN 11 20 Poly-Pro.
 FT DOMAIN 256 262 Calcineurin B binding-site 1 (Potential).
 FT DOMAIN 305 310 Calcineurin B binding-site 2 (Potential).
 FT DOMAIN 402 424 Calmodulin-binding (Potential).
 FT DOMAIN 475 497 Inhibitory domain.
 FT METAL 99 99 Iron (By similarity).
 FT METAL 101 101 Iron (By similarity).
 FT METAL 127 127 Iron and zinc (By similarity).
 FT METAL 159 159 Zinc (By similarity).
 FT ACT SITE 160 160 Proton donor (By similarity).
 FT METAL 208 208 Zinc (By similarity).
 FT METAL 290 290 Zinc (By similarity).
 SQ SEQUENCE 525 AA; 59113 MW; 5E66AF3100BE3987 CRC64;

Query Match 86.2%; Score 2370; DB 1; Length 525;
 Best Local Similarity 95.4%; Pred. No. 2.2e-171;
 Matches 453; Conservative 1; Mismatches 1; Indels 20; Gaps 3;

QY 1 MAAPPARAAAPPPPPPPPPGADRVKAVKAVPPPPHRLTSEVFDLGI PRVDVLKHLV 60
 DB 1 MAAPPARAAAPPPPPPPPPGADRVKAVKAVPPPPHRLTSEVFDMDGIPRVVDLKHLV 60

QY 61 KEGRVDEIALRIINEGAAILRREKTMIEVEAPITVCGDIHQGFDMKLFVGGSPANT 120
 DB 61 KEGRVDEIALRIINEGAAILRREKTMIEVEAPITVCGDIHQGFDMKLFVGGSPANT 120

QY 121 RYFLGDYVDRGYFSIEHVLGTEDISINPHNNIECVLYLWLVKILYPSITLFLLRGNHE 180
 DB 121 RYFLGDYVDRGYFSI-----ECVLYLWLVKILYPSITLFL-LLRGNHE 161

QY 181 CRHLYTEYTFKQECKIKYSERYVEACMEAPDSLPALALNQOFLCVHGLSPETHLDDI 240
 DB 162 CRHLYTEYTFKQECKIKYSERYVEACMEAPDSLPALALNQOFLCVHGLSPETHLDDI 221

QY 241 RRLDRFKEPPAFGPMCDLLWSDPSDFGNEKSEQHFSHTVGRGCSFYFNPVAVCEFLQNN 300
 DB 222 RRLDRFKEPPAFGPMCDLLWSDPSDFGNEKSEQHFSHTVGRGCSFYFNPVAVCEFLQNN 281

QY 301 NLLSIIRAHAQDAGYRMYRSQTTGFPPLITIFSAPNYLDVYNNKAAVLKYENNVNMR 360
 DB 282 NLLSIIRAHAQDAGYRMYRSQTTGFPPLITIFSAPNYLDVYNNKAAVLKYENNVNMR 341

QY 361 QFNCSPHYPLNFMNDVFTWSLPFVGEKVTMLVNLVSLICSDDELMTGEDEQDFD-GSAAA 419
 DB 342 QFNCSPHYPLNFMNDVFTWSLPFVGEKVTMLVNLVSLICSDDELMTGEDEQDFDVGSA 401

QY 420 RKEIIRNKIRAIKGMARVSVLRESESVTLKGLTPTGMLPSGVLAGGRTQLQS 474
 DB 402 RKEIIRNKIRAIKGMARVSVLRESESVTLKGLTPTGMLPSGVLAGGRTQLQS 456

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Db 282 NLLSIIIRAHAQDAGYMYRKSQTGTGPFSLTIFSAAPNYLDVYNNKAVALKYENNVNIR 341
Qy 361 QFNCSPHYWLPNFMVDVFTWSLPLPVGKVTETMLVNVLSICSDDELMTGEGDQFD-GSAAA 419
Db 342 QFNCSPHYWLPNFMVDVFTWSLPLPVGKVTETMLVNVLSICSDDELMTGEGDQFDVGSA 401
Qy 420 RKEIIRNKIRAIKQKARVSVLRESESVLTGKLTPTGMLPSGVLAGGRQTLS 474
Db 402 RKEIIRNKIRAIKQKARVSVLRESESVLTGKLTPTGMLPSGVLAGGRQTLS 456

RESULT 7
Q7TIF5
ID Q7TIF5 PRELIMINARY; PRT; 504 AA.
AC Q7TIF5;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Calciurein A alpha (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Liberatore C.M., Yutzev K.E.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
    phosphate.
CC -1- SIMILARITY: Belongs to the PPP phosphatase family.
DR EMBL; AY242434; AAF92382.1; -.
DR HSP; Q08209; IAU1.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR InterPro; IPR004843; M:pesterase.
DR Pfam; PF00149; Metallophos_1_apah.
DR ProDom; PD000252; T_phatase_apah; 1.
DR SMART; SM00156; PP2AC; 1.
DR PROSITE; PS00125; SER_THR_PHOSPHATASE; UNKNOWN_1.
FT NON TER 1
SQ SEQUENCE 504 AA; 56913 MW; 17964C2818765BC5 CRC64;

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Query Match 74.9%; Score 2060.5; DB 2; Length 504;
Best Local Similarity 85.4%; Pred. No. 6.8e-148;
Matches 386; Conservative 33; Mismatches 12; Indels 21; Gaps 4;

Qy 24 DRVVKAVFPPTHLTSEVFDLDGIPRVDVKNHLYKEGRVDEIALLRIINGAAILRR 83
Db 9 DRVVKAVFPPTSHRLTAKEVFDNDGKPRVDILKAHLMKEGRLEESVALRIITEGASILRQ 68

Qy 84 EKTMIIEAPITVCGDIGHGQFFDLMLKLFVEGGSPANTRYFLGDYVDRGFSEIHLVLTGE 143
Db 69 EKLLDIDAPVTVCGDIGHGQFFDLMLKLFVEGGSPANTRYFLGDYVDRGFSEI----- 121

Qy 144 DISINPHNNNECVLYLWVILKILYPTSLFLLRGNHECRHLTEYFTFKQCKIKYSRVY 203
Db 122 -----ECVLYLWALKILYPTKTLF-LLRGNHECRHLTEYFTFKQCKIKYSRVY 169

Qy 204 EACWEAFDSLPLAALLNQOFLCVHGGSLPEIHTLDDIRLDRFKEPPAFGPMCDLLWSDP 263
Db 170 DACMDAFDCIPLAALMNQOFLCVHGGSLPEINTLDDIRKLDRFKEPPAYFGMCDILWSDP 229

Qy 264 SEDFGNEKSOEHFSHTNVRGCSFYFNYPVACEFLONNLLSIIRAHAQDAGYMYRKSQ 323
Db 230 LEDFGNEKTOEHFTNVRGCSFYFYPVACEFLOHNNLLSILRAHAQDAGYMYRKSQ 289

Qy 324 TTGFPSSLITIFSAAPNYLDVYNNKAVALKYENNVNIRQFNCSPHYWLPNFMVDVFTWSL 383
Db 290 TTGFPSSLITIFSAAPNYLDVYNNKAVALKYENNVNIRQFNCSPHYWLPNFMVDVFTWSL 349

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Qy 384 FVGEKVTETMLVNVLSICSDDELMTGEGDQFDG-SAAARKEIIRNKIRAIKQKARVSVL 442
Db 350 FVGEKVTETMLVNVLSICSDDELGTE-EDGFDGATAARKEIIRNKIRAIKQKARVSVL 408

Qy 443 EESESVLTGKLTPTGMLPSGVLAGGRQTLS 474
Db 409 EESESVLTGKLTPTGMLPSGVLAGGRQTLS 440

RESULT 8
Q8TAW9
ID Q8TAW9 PRELIMINARY; PRT; 511 AA.
AC Q8TAW9;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE PPP3CA protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Pancreas;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Raheij J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
    and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Pancreas;
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
    phosphate.
CC -1- SIMILARITY: Belongs to the PPP phosphatase family.
DR EMBL; BC025714; AAH25714.1; -.
DR HSP; Q08209; IIM63.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR InterPro; IPR004843; M:pesterase.
DR InterPro; IPR006186; T_phatase_apah.
DR Pfam; PF00149; Metallophos; 1.
DR PRINTS; PR00114; STPHPTASE.
DR ProDom; PD000252; T_phatase_apah; 1.
DR SMART; SM00156; PP2AC; 1.
DR PROSITE; PS00125; SER_THR_PHOSPHATASE; UNKNOWN_1.
DR Hydrolase; Iron.
SQ SEQUENCE 511 AA; 57658 MW; B1E98CC0D6034CCC CRC64;

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Query Match 74.8%; Score 2057.5; DB 2; Length 511;
Best Local Similarity 83.8%; Pred. No. 1.2e-147;
Matches 387; Conservative 34; Mismatches 21; Indels 21; Gaps 4;

Qy 13 PPPPPPPPGADRVKAVFPPTHLTSEVFDLDGIPRVDVKNHLYKEGRVDEIALLR 72
Db 4 PKAIDPKLSTTDVVKAVFPPTSHRLTAKEVFDNDGKPRVDILKAHLMKEGRLEESVALR 63

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QY 133 YFSIEHVLGTEDISINPHNNINECVLYLWVLKILYPSLFLLLRGNHCHRLTEYFTPKQ 192
DB 124 YFSI-----ECVLYLWALKILYPKTLF-LLRGNHCHRLTEYFTPKQ 164
QY 193 ECKIKYSRVYEAACMEAFDSLPLAALLNQOFLCVHGGLSPEIHTLDDIRRLDRFKPEPPAF 252
DB 165 ECKIKYSRVYDACHADFCLPLAALMNQOFLCVHGGLSPEINTLDDIRKLDRFKPEPPAY 224
QY 253 GPMCDLLWSDPSDFGNEKSQEHFSHNTVRGCSYFYNYPAVCEFLQNNLLSIIRAHEAQ 312
DB 225 GPMCDLLWSDPLEDFGNEKTQEHFTHTVTRGCSYFYSPAVCEFLQNNLLSILRAHEAQ 284
QY 313 DAGYRMYRKSQTTGPPSLITIFSAFNLYLDVNNKAAVLKYENNVMNIQFNCSPHPYWLP 372
DB 285 DAGYRMYRKSQTTGPPSLITIFSAFNLYLDVNNKAAVLKYENNVMNIQFNCSPHPYWLP 344
QY 373 NFMDFVFTWSLFPVGEKVTMELVNVLSICSDDELMTGEDQFDG-SAAARKEIIRNKIRAI 431
DB 345 NFMDFVFTWSLFPVGEKVTMELVNVLSICSDDELGSE-EDGFDGATAARKEVIRNKIRAI 403
QY 432 GKMARVFSVLRESESVLTLKGLTPTGMLPSGVLGAGRTQLQS 474
DB 404 GKMARVFSVLRESESVLTLKGLTPTGMLPSGVLGAGRTQLQS 446

RESULT 9
Q8HZN0
ID Q8HZN0 .PRELIMINARY; PRT; 511 AA.
AC Q8HZN0;
DT 01-MAR-2003 (TRENDELrel. 23, Created)
DT 01-MAR-2003 (TRENDELrel. 23, Last sequence update)
DE Calcieneurin A alpha.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22443975; PubMed=12419772;
RA Sun L., Moonga B.S., Lu M., Zaidi N., Iqbal J., Blair H.C.,
RA Epstein S., Abe E., Troen B.R., Huang C.L.H., Zaidi M.;
RT "Molecular cloning, expression, and function of osteoclastic
RL Am. J. Physiol. Renal Physiol. 284:F575-F583(2003).
CC -1- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
CC phosphate.
CC -1- SIMILARITY: Belongs to the PPP phosphatase family.
DR EMBL; AF541960; AAN23152.1; -.
DR HSSP; Q08209; IMG3.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR InterPro; IPR004843; M:pesterase.
DR InterPro; IPR006186; T:phatase_apah.
DR Pfam; PF00149; Metallophos; 1.
DR PRINTS; PR00114; STPHPTASE.
DR PRODOM; PD000252; T_phatase_apah; 1.
DR SMART; SM00156; PP2Ac; 1.
DR PROSITE; PS00125; SER_THR_PHOSPHATASE; UNKNOWN_1.
KW Hydrolase; Itron.
SQ SEQUENCE 511 AA; 57655 MW; B1P28D70C7F34CCC CRC64;

Query Match 74.8%; Score 2057.5; DB 2; Length 511;
Best Local Similarity 83.6%; Pred. No. 1.2e-147;
Matches 387; Conservative 34; Mismatches 21; Indels 21; Gaps 4;

QY 13 PPPPPPPGADRVVKAVPFPPTHLTSEEVFDLGIIPRDVVLKHLVKEGRVDEIRALR 72
DB 4 PRAIDPKLSTTDRVVVKAVPFPFPSHRLTAKEVPFNDGKPRVDILKAHLMKEGRLEESVALR 63

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QY 73 IINEGAAILRREKTMIEVEAPITVCGDIHGQFFDLMLKLFVGGSPANTRYILFLGDYVDRG 132
DB 64 IITEGASILRQEKNLDDIDAPVTVCGDIHGQFFDLMLKLFVGGSPANTRYILFLGDYVDRG 123
QY 133 YFSIEHVLGTEDISINPHNNINECVLYLWVLKILYPSLFLLLRGNHCHRLTEYFTPKQ 192
DB 124 YFSI-----ECVLYLWALKILYPKTLF-LLRGNHCHRLTEYFTPKQ 164
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DB 225 GPMCDLLWSDPLEDFGNEKTQEHFTHTVTRGCSYFYSPAVCEFLQNNLLSILRAHEAQ 284
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DB 285 DAGYRMYRKSQTTGPPSLITIFSAFNLYLDVNNKAAVLKYENNVMNIQFNCSPHPYWLP 344
QY 373 NFMDFVFTWSLFPVGEKVTMELVNVLSICSDDELMTGEDQFDG-SAAARKEIIRNKIRAI 431
DB 345 NFMDFVFTWSLFPVGEKVTMELVNVLSICSDDELGSE-EDGFDGATAARKEVIRNKIRAI 403
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P2BA HUMAN
ID P2BA HUMAN STANDARD; PRT; 521 AA.
AC Q08209;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Serine/threonine protein phosphatase 2B catalytic subunit, alpha
DE isoform (BC 3.1.3.16) (Calmodulin-dependent calcineurin A subunit,
DE alpha isoform) (CAM-PRP catalytic subunit).
GN Name=PPP3CA; Synonyms=CALNA, CNA;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Brain;
RX MEDLINE=93320118; PubMed=8392375; DOI=10.1016/0167-4889(93)90117-8;
RA Muramatsu T., Kincaid R.L.;
RT "Molecular cloning of a full-length cDNA encoding the catalytic
RT subunit of human calmodulin-dependent protein phosphatase (calcineurin
RT A alpha).";
RL Biochim. Biophys. Acta 1178:117-120(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX TISSUE=Amalgam;
RA Ansonge W., Wirkner U., Mewes H.-W., Weil B., Wiemann S.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
RX MEDLINE=96097077; PubMed=8524402; DOI=10.1038/378641a0;
RA Kisinger C.R., Parge H.E., Knighton D.R., Lewis C.T., Pelletier L.A.,
RA Tempczyk A., Kalish V.J., Tucker K.D., Showalter R.E., Moomaw E.W.,
RA Gasconet L.N., Habuka N., Chen X., Maldonado F., Barker J.E.,
RA Bacquet R., Villafranca J.E.;
RT "Crystal structures of human calcineurin and the human FKBP12-PK506-
RT calcineurin complex.";
RL Nature 378:641-644(1995).
CC -1- FUNCTION: Calcium-dependent, calmodulin-stimulated protein
CC phosphatase. This subunit may have a role in the calmodulin
CC activation of calcineurin.
CC -1- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +

```

phosphate.
 -1- COFACTOR: Binds 1 iron(III) ion and 1 zinc ion per subunit.
 -1- SUBUNIT: Composed of two components (A and B), the A component is the catalytic subunit and the B component confers calcium sensitivity.
 -1- SIMILARITY: Belongs to the PPP phosphatase family. PP-2B subfamily.

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 EMBL; L14778; AAA02631.1; -;
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 PIR; S35067; S35067.
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 PDB; 1MF8; X-ray; A=20-392.
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 MIM; 114105; -;
 GO; GO:0005955; C:calcineurin complex; NAS.
 GO; GO:0005909; F:calcium ion binding; NAS.
 GO; GO:0005516; F:calmodulin binding; NAS.
 GO; GO:0004722; F:protein serine/threonine phosphatase activity; NAS.
 GO; GO:0006470; P:protein amino acid dephosphorylation; NAS.
 InterPro; IPR004843; M-pesterase.
 InterPro; IPR006186; T_phatase_apah.
 Pfam; PF00149; Metallophos; 1.
 PRINTS; PR00114; STPHPTASE.
 ProDom; PD000252; T_phatase_apah; 1.
 SMART; SM00156; PP2Ac; 1.
 PROSITE; PS00125; SER_THR_PHOSPHATASE; 1.
 3D-structure; Calmodulin-binding; Hydrolase; Iron; Metal-binding;
 Multigene family; Protein phosphatase; Zinc.
 DOMAIN 1 301 Catalytic.
 FT DOMAIN 247 253 Calcineurin B binding-site 1 (Potential).
 FT DOMAIN 296 301 Calcineurin B binding-site 2 (Potential).
 FT DOMAIN 392 414 Calmodulin-binding (Potential).
 FT DOMAIN 465 487 Inhibitory domain.
 FT METAL 90 90 Iron.
 FT METAL 92 92 Iron.
 FT METAL 118 118 Iron and zinc.
 FT METAL 150 150 Zinc.
 FT METAL 199 199 Zinc.
 FT METAL 281 281 Zinc.
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 Query Match 74.8%; Score 2057.5; DB 1; Length 521;
 Best Local Similarity 83.6%; Pred. No. 1.2e-147;
 Matches 387; Conservative 34; Mismatches 21; Indels 21; Gaps 4;

 QY 13 PPPPPPPGADRVKAVPPPPPHRLTSEVFOLDGI PRVDVILKNHLVKGRVDEEIALR 72
 DB 4 PKAIDPKLSTTDVVKAVPPPPSHRLTAKEVFONDGKPRVDILKAHLMEGRLEESVALR 63
 QY 73 IINEGRAILRRKTMIEVEAPITVCGDIHQFFDLMLKEVGGSPANTRYFLGDDVYDRG 132
 DB 64 IITEGASILKQEKNNLLDIDAPVTVCGDIGHQFFDLMLKEVGGSPANTRYFLGDDVYDRG 123
 QY 133 YFSIEHVLGTEDISINPHNNINECVLYLWVLKILYPTSTFLLLRGNHCEHRLTEYFTFKQ 192
 DB 124 YFSI-----ECVLYLWALKILYPTLF-LLRGNHCEHRLTEYFTFKQ 164
 QY 193 ECKIKYSERYEACMEAFDLSPLAALLNQOFLCVHGGLSPEIHTLDDIRLDRFKPEPPAF 252
 DB 165 ECKIKYSERYDADCFDCLPLAALMNQOFLCVHGGLSPEINTLDDIRLDRFKPEPPAY 224
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 DB 225 GPMCDLLWSDPLEDFGNEKTQEHFTNTVRGCSYFYNYPAVCFEFLQNNLLSIIIRAHEAQ 284
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 DB 285 DAGYMYRKSQTTGFPFSLITIFSAPNYLDVYNNKAAVLKYNNVMNIRQNCSPHPYWLP 344
 QY 373 NFMDVFTWSLPFVGEKVTMLNVNLSICSDDELMTEGEOQFDG-SAAARKEIIRNKIRAI 431
 DB 345 NFMDVFTWSLPFVGEKVTMLNVNLSICSDDELMTEGEOQFDG-EDGFDGATAAARKEIIRNKIRAI 403
 QY 432 GKMARVFSVLRRESESVLTILKGLTPTGMLPSGVLAGSGROTLOS 474
 DB 404 GKMARVFSVLRRESESVLTILKGLTPTGMLPSGVLAGSGKQTLOS 446

 RESULT 11
 P2BA_BOVIN

P2BA BOVIN STANDARD; PRT; 521 AA.
P48452;
AC 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Serine/threonine protein phosphatase 2B catalytic subunit, alpha
DE isoform (EC:3.1.3.16) [Calmodulin-dependent calcineurin A subunit,
DE alpha isoform] (CAM-PRP catalytic subunit).
GN Name=PPP3CA;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A., AND X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
RC TISSUE=Brain;
RX MEDLINE=95360994; PubMed=7543369; DOI=10.1016/0092-8674(95)90439-5;
RA Griffith J.P., Kim J.L., Kim E.E., Sintchak M.D., Thomson J.A.,
RA Fitzgibbon M.J., Fleming M.A., Caron P.R., Hsiao K., Navia M.A.;
RT "X-ray structure of calcineurin inhibited by the immunophilin-
RT immunosuppressant FKBP12-FK506 complex."; Cell 82:507-522(1995).
RL Cell 82:507-522(1995).
CC -!- FUNCTION: Calcium-dependent, calmodulin-stimulated protein
CC phosphatase. This subunit may have a role in the calmodulin
CC activation of calcineurin.
CC -!- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
CC phosphate.
CC -!- COFACTOR: Binds 1 iron(III) ion and 1 zinc ion per subunit.
CC -!- SUBUNIT: Composed of two components (A and B), the A component is
CC the catalytic subunit and the B component confers calcium
CC sensitivity.
CC -!- SIMILARITY: Belongs to the PPP phosphatase family. PP-2B
CC subfamily.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
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CC EMBL; U33868; AAC48473.1; -;
CC PIR; A56968; A56968.
CC PDB; LTCO; X-ray; A-18-392.
CC InterPro; IPR004843; M-pesterase.
CC DR Pfam; PF00149; Metallophos; 1.
CC DR PRINTS; PR00114; STPHPTASE.
CC DR ProDom; PD000252; T.phase_apah; 1.
CC DR SMART; SM00156; PP2Ac; 1.
CC DR PROSITE; PS00125; SER_THR_PHOSPHATASE; 1.
CC 3D-structure; Calmodulin-binding; Hydrolase; Iron; Metal-binding;
CC Multigene family; Protein phosphatase; Zinc.
CC DOMAIN 1 301 Catalytic.
CC FT DOMAIN 247 253 Calcineurin B binding-site 1 (Potential).
CC FT DOMAIN 296 301 Calcineurin B binding-site 2 (Potential).
CC FT DOMAIN 392 404 Calmodulin-binding (Potential).
CC FT DOMAIN 465 487 Inhibitory domain.
CC FT METAL 90 90 Iron.
CC FT METAL 92 92 Iron.
CC FT METAL 118 118 Iron and zinc.
CC FT METAL 150 150 Zinc.
CC FT METAL 199 199 Zinc.
CC FT METAL 281 281 Zinc.
CC FT STRAND 29 29
CC FT HELIX 31 34
CC FT STRAND 35 35
CC FT TURN 37 38
CC FT STRAND 41 41
CC FT STRAND 43 51
CC FT HELIX 52 53
CC TURN 52 53

56 56 74.8%; Score 2056.5; DB 1; Length 521;
58 58 83.6%; Pred. No. 1.4e-147;
78 78 387; Conservative 34; Mismatches 21; Indels 21; Gaps 4;
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Best Local Similarity 74.8%; Score 2056.5; DB 1; Length 521;
Matches 387; Conservative 34; Mismatches 21; Indels 21; Gaps 4;
QY 13 PPPPPPPPGADRVVKKAVPPPPHRLTSEEVFDLDGIPRVDLKHLVKEGRVDEIALR 72
DB 4 PKADPKSLTTRDVVKKAVPPPPSHRLTAKEVFDNDGKPRVDILKAHLMEGRLEETVALR 63
QY 73 IINGGAAILREKTMIEVEAPITVCGDHGFFDLMKLFVGGSPANTRYILFGDYVDRG 132
DB 64 IITEGASILROEKNLDDIDAPVTVCGDTHGFFDLMKLFVGGSPANTRYILFGDYVDRG 123
QY 133 YFSIEHVLGTEDISINPHNNINECVLYLWLVKLYPSTFLLLRGNHCRHLTEYFTPKQ 192
DB 124 YFSI-----ECVLYLWLVKLYPSTFLLLRGNHCRHLTEYFTPKQ 164
QY 193 ECKIKYSERVYEAQWEAFDSLPALALNQQLCVHGGSLSPHITLDDIRRLDRFKPEPPAF 252
DB 165 ECKIKYSERVYDADCAFDCLPLAALNQQLCVHGGSLSPHITLDDIRKLDRFKPEPAY 224
QY 253 GPMCDLLWSDPSEDFGNEKSGHFSHNTVRCGSFYFNYPAVCEFLQNNLLSILRAHAQ 312
DB 225 GPMCDLLWSDPLEDFGNEKTQEHFTHTVRCGSFYFNYPAVCEFLQNNLLSILRAHAQ 284

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QY 373 NFMDVFTWSLPFVGEKVTMLVNVLSICSDDELMTEGEDQFDG-SAAARKEIIRNKIRAI 431
Db 345 NFMDVFTWSLPFVGEKVTMLVNVLSICSDDELGSE-EDGFDGATAARKEIIRNKIRAI 403
QY 432 GKMARVSVLREESVSLTKGLTPTGMLPSGVLAGGRTQLQS 474
Db 404 GKMARVSVLREESVSLTKGLTPTGMLPSGVLAGGRTQLQS 446

RESULT 12
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AC Q9WUV7
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Serine/threonine specific protein phosphatase (EC 3.1.3.16).
GN Names=calcineurin A gene;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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RC STRAIN=Sprague-Dawley; TISSUE=Antire brain;
RX MEDLINE=92348467; PubMed=1322410;
RA Perrinoo B.A., Fong Y.L., Brickey D.A., Saitoh Y., Ushio Y.,
RA Fukunaga K., Miyamoto E., Soderling T.R.;
RT "Characterization of the phosphatase activity of a Baculovirus-
expressed calcineurin A isoform.";
RL J. Biol. Chem. 267:15965-15969(1992).
CC -I- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
phosphate.
CC -I- SIMILARITY: Belongs to the PPP phosphatase family.
DR EMBL; X57115; CAA0398.2; -.
DR HSP; Q08209; IM63.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR InterPro; IPR004721; F:phosphoprotein phosphatase activity; IEA.
DR InterPro; IPR004843; N-pesterase.
DR InterPro; IPR006186; T_phase_apah.
DR Pfam; PF00149; Metallophos; 1.
DR PRINTS; PR00114; STPHPHASE.
DR PRODOM; PD000252; T_phase_apah; 1.
DR SMART; SM00156; PP2AC; 1.
DR PROSITE; PS00125; SER_THR_PHOSPHATASE; UNKNOWN_1.
KW Hydrolase; Iron.
SQ SEQUENCE 511 AA; 57614 MW; 01428D70D674508D CRC64;

Query Match 74.7%; Score 2054.5; DB 2; Length 511;
Best Local Similarity 83.4%; Pred. No. 2e-147;
Matches 386; Conservative 35; Mismatches 21; Indels 21; Gaps 4;

QY 13 PPPPPPPPGADRVKAVPPPPHRLTSEVFDLGIIPVDVLKNHLVKEGRVDEIALR 72
Db 4 PKAIDPKLSTTDVVKAVPPPPSHRLTAKEVFNDGKPRVDILKAHLMEGRLEESVALR 63
QY 73 IINEGAAILREKTMIEVEAPITVCGDIHQGFEDLMKLFVGGSPANTRYFLGDIYDRG 132
Db 64 IITEGASILRQENLLDIDAPVTVCGDIHQGFEDLMKLFVGGSPANTRYFLGDIYDRG 123
QY 133 YFSIEHVLGTEDISINPHNNINECVLYLWLKILYPTSLFLLRGNHCEHRLTEYFTFKQ 192
Db 124 YFSI-----ECVLYLWALKILYPKTLF-LLRGNHCEHRLTEYFTFKQ 164
QY 193 ECKIKYSERYVACMEAFDLSPLAALNQOFLCVHGGLSPEIHTLDDIRLDRFKPEPPAF 252
Db 165 ECKIKYSERYVACMDAFDCLPLAALNQOFLCVHGGLSPEINTLDDIRLDRFKPEPPAY 224

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QY 253 GPMCDLLWSDPSDFGNEKSQEHFSHNTVRGCSFYFYNYPACVCFLONNLLSIRAHEAQ 312
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QY 313 DAGYMRKSTQTTGFPSSLITIFSAAPNYLDVYNNKAAVLKYENNVMNIRQNCSPHPYWLP 372
Db 285 DAGYMRKSTQTTGFPSSLITIFSAAPNYLDVYNNKAAVLKYENNVMNIRQNCSPHPYWLP 344
QY 373 NFMDVFTWSLPFVGEKVTMLVNVLSICSDDELMTEGEDQFDG-SAAARKEIIRNKIRAI 431
Db 345 NFMDVFTWSLPFVGEKVTMLVNVLSICSDDELGSE-EDGFDGATAARKEIIRNKIRAI 403
QY 432 GKMARVSVLREESVSLTKGLTPTGMLPSGVLAGGRTQLQS 474
Db 404 GKMARVSVLREESVSLTKGLTPTGMLPSGVLAGGRTQLQS 446

RESULT 13
P2BA_MOUSE
ID P2BA_MOUSE STANDARD; PRT; 521 AA.
AC P83328; P12816; P20652;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DE Serine/threonine protein phosphatase 2B catalytic subunit, alpha
isoform (EC 3.1.3.16) (Calmodulin-dependent calcineurin A subunit,
alpha isoform) (CAM-PRP catalytic subunit).
GN Names=Ppp3ca; Synonyms=Calna;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=90293081; PubMed=2162844;
RA Kincaid R.L., Giri P.R., Higuchi S., Tamura J., Dixon S.C.,
RA Marietta C.A., Amoresse D.A., Martin B.M.;
RT "Cloning and characterization of molecular isoforms of the catalytic
subunit of calcineurin using nonisotopic methods.";
RL J. Biol. Chem. 265:11312-11319(1990).
RN [2]
SEQUENCE OF 215-521 FROM N.A.
RX MEDLINE=89057863; PubMed=2848250;
RA Kincaid R.L., Nightingale M.S., Martin B.M.;
RT "Characterization of a cDNA clone encoding the calmodulin-binding
domain of mouse brain calcineurin.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:8983-8987(1988).
RN [3]
SEQUENCE OF 95-116 FROM N.A.
RX MEDLINE=94357899; PubMed=8077208;
RA Becker W., Kentrup H., Klumpp S., Schultz J.E., Joost H.G.;
RT "Molecular cloning of a protein serine/threonine phosphatase
containing a putative regulatory tetratricopeptide repeat domain.";
RL J. Biol. Chem. 269:22586-22592(1994).
CC -I- FUNCTION: Calcium-dependent, calmodulin-stimulated protein
phosphatase. This subunit may have a role in the calmodulin
activation of calcineurin.
CC -I- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
phosphate.
CC -I- COFACTOR: Binds 1 iron(III) ion and 1 zinc ion per subunit (By
similarity).
CC -I- SUBUNIT: Composed of two components (A and B), the A component is
the catalytic subunit and the B component confers calcium
sensitivity.
CC -I- SIMILARITY: Belongs to the PPP phosphatase family. PP-2B
subfamily.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
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entities requires a license agreement (See http://www.isb-sib.ch/announce/)

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or send an email to license@isb-sib.ch).
CC EMBL; J05479; AAA37359.1; -.
DR EMBL; J04134; AAA37432.1; -.
DR PIR; A42232; A31257.
DR HSSP; Q08209; 1M63.
DR MGD; MGI:107164; Ppp3ca.
DR InterPro; IPR004843; M-pesterase.
DR Pfam; PF006186; T_phase_apah.
DR PRINTS; PR00114; STPHPTASE.
DR PRODOM; PD000252; T_phase_apah; 1.
DR SMART; SM00156; Pp2Ac; 1.
DR PROSITE; PS00125; SER_THR_PHOSPHATASE; 1.
KW Calmodulin-binding; Hydrolase; Iron; Metal-binding; Multigene family;
KW Protein phosphatase; Zinc.
FT DOMAIN 1 301 Catalytic.
FT DOMAIN 247 253 Calcineurin B binding-site 1 (Potential).
FT DOMAIN 296 301 Calcineurin B binding-site 2 (Potential).
FT DOMAIN 392 414 Calmodulin-binding (Potential).
FT DOMAIN 465 487 Inhibitory domain.
FT METAL 90 90 Iron (By similarity).
FT METAL 92 92 Iron (By similarity).
FT METAL 118 118 Iron and zinc (By similarity).
FT METAL 150 150 Zinc (By similarity).
FT ACT SITE 151 151 Proton donor (By similarity).
FT METAL 199 199 Zinc (By similarity).
FT METAL 281 281 Zinc (By similarity).
SQ SEQUENCE 521 AA; 58643 MW; 16530C27DDBF1F05 CRC64;

Query Match 74.7%; Score 2054.5; DB 1; Length 521;
Best Local Similarity 83.4%; Pred. No. 2e-147;
Matches 386; Conservative 35; Mismatches 21; Indels 21; Gaps 4;

Qy 13 PPPPPPPGADRVVKA VPPPTT HRLTSEE VFDLGI PRVDV LK N H L V K E G R V D E I A L R 72
Db 4 PKAIDPKLSTTDRVVVKA VPPPTT HRLTSEE VFDLGI PRVDV LK N H L V K E G R V D E I A L R 63

Qy 73 IINEGAALREKTMIEVAPITTCGDITHGQFFDLMLKLFVGGSPANTRYLFLGDYVDRG 132
Db 64 IITEGASILRQEKLLDIDAPVTCGDITHGQFFDLMLKLFVGGSPANTRYLFLGDYVDRG 123

Qy 133 YFSIEHVLGTEDISINPHNNIECVLYLWLKILYPTSLFLLLRGNHECHRLTYEFTFKQ 192
Db 124 YFSI-----ECVLYLWLKILYPTKTLF-LLRGNHECHRLTYEFTFKQ 164

Qy 193 ECKIYSERVYEAWEAFDSPLAALLNQFLCVHGGLSPEIHTLDDIRLDRFKPEPPAF 252
Db 165 ECKIYSERVYDADWDADFCLPLAALMNQFLCVHGGLSPEINTLDDIRLDRFKPEPPAY 224

Qy 253 GPMCDLLWSDSEDFGNEKSOEHFHNVTVCGSFYFNPVPAVCEFLQNNLLSIIRAHEAQ 312
Db 225 GPMCDLLWSDLEDFGNEKTEQHEFHNVTVCGSFYFNPVPAVCEFLQNNLLSIIRAHEAQ 284

Qy 313 DAGYMYRKSQTTGPPSLITIFSAFNLYDVNNKAAVLKYNNVNNIQQFNCSPHYWLP 372
Db 285 DAGYMYRKSQTTGPPSLITIFSAFNLYDVNNKAAVLKYNNVNNIQQFNCSPHYWLP 344

Qy 373 NFMVDVFTWSLFPVGEKVETMLVNVLISICSDDELMTGEDQFDG-SAAARKKIIIRNKIRAI 431
Db 345 NFMVDVFTWSLFPVGEKVETMLVNVLISICSDDELMTGEDQFDG-SAAARKKIIIRNKIRAI 403

Qy 432 GKMARVFSVLRESESVLTGLTPTGMLPSGLVLAGGQTLOS 474
Db 404 GKMARVFSVLRESESVLTGLTPTGMLPSGLVLAGGQTLOS 446

RESULT 14
P2BA_RAT
ID P2BA_RAT STANDARD; PRT; 521 AA.
AC P63329; P12816; P20652;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)

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25-OCT-2004 (Rel. 45, Last annotation update)
Serine/threonine protein phosphatase 2B catalytic subunit, alpha isoform (EC 3.1.3.16) (Calmodulin-dependent calcineurin A subunit, alpha isoform) (CAM-PRP catalytic subunit).
Name=Ppp3ca; Synonyms=Calna;
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
[1]
SEQUENCE FROM N.A.
MEDLINE=89392066; PubMed=2551293;
Ito A., Hashimoto T., Hirai M., Takeda T., Shuntoh H., Kuno T., Tanaka C.;
"The complete primary structure of calcineurin A, a calmodulin binding protein homologous with protein phosphatases 1 and 2A.";
Biochem. Biophys. Res. Commun. 163:1492-1497(1989).
-!- FUNCTION: Calcium-dependent, calmodulin-stimulated protein phosphatase. This subunit may have a role in the calmodulin activation of calcineurin.
-!- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein + phosphates. Binds 1 iron(III) ion and 1 zinc ion per subunit (By similarity).
-!- COFACTOR: Binds 1 iron(III) ion and 1 zinc ion per subunit (By similarity). Composed of two components (A and B), the A component is the catalytic subunit and the B component confers calcium sensitivity (By similarity).
-!- SIMILARITY: Belongs to the PPP phosphatase family. PP-2B subfamily.
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EMBL; M29275; AAA40940.1; -.
EMBL; D90035; BAA14083.1; -.
PIR; A33264; A33264.
HSSP; Q08209; 1M63.
RGD; 3382; Ppp3ca.
InterPro; IPR004843; M-pesterase.
InterPro; IPR006186; T_phase_apah.
Pfam; PF00149; Metallophos; 1.
PRINTS; PR00114; STPHPTASE.
PRODOM; PD000252; T_phase_apah; 1.
SMART; SM00156; Pp2Ac; 1.
PROSITE; PS00125; SER_THR_PHOSPHATASE; 1.
Calmodulin-binding; Hydrolase; Iron; Metal-binding; Multigene family;
Protein phosphatase; Zinc.
KW DOMAIN 1 301 Catalytic.
KW DOMAIN 247 253 Calcineurin B binding-site 1 (Potential).
KW DOMAIN 296 301 Calcineurin B binding-site 2 (Potential).
KW DOMAIN 392 414 Calmodulin-binding (Potential).
KW DOMAIN 465 487 Inhibitory domain.
KW METAL 90 90 Iron (By similarity).
KW METAL 92 92 Iron (By similarity).
KW METAL 118 118 Iron and zinc (By similarity).
KW METAL 150 150 Zinc (By similarity).
KW ACT SITE 151 151 Proton donor (By similarity).
KW METAL 199 199 Zinc (By similarity).
KW METAL 281 281 Zinc (By similarity).
SQ SEQUENCE 521 AA; 58643 MW; 16530C27DDBF1F05 CRC64;

Query Match 74.7%; Score 2054.5; DB 1; Length 521;
Best Local Similarity 83.4%; Pred. No. 2e-147;
Matches 386; Conservative 35; Mismatches 21; Indels 21; Gaps 4;

Qy 13 PPPPPPPGADRVVKA VPPPTT HRLTSEE VFDLGI PRVDV LK N H L V K E G R V D E I A L R 72
Db 4 PKAIDPKLSTTDRVVVKA VPPPTT HRLTSEE VFDLGI PRVDV LK N H L V K E G R V D E I A L R 63

Qy 73 IINEGAALREKTMIEVAPITTCGDITHGQFFDLMLKLFVGGSPANTRYLFLGDYVDRG 132
Db 64 IITEGASILRQEKLLDIDAPVTCGDITHGQFFDLMLKLFVGGSPANTRYLFLGDYVDRG 123

Qy 133 YFSIEHVLGTEDISINPHNNIECVLYLWLKILYPTSLFLLLRGNHECHRLTYEFTFKQ 192
Db 124 YFSI-----ECVLYLWLKILYPTKTLF-LLRGNHECHRLTYEFTFKQ 164

Qy 193 ECKIYSERVYEAWEAFDSPLAALLNQFLCVHGGLSPEIHTLDDIRLDRFKPEPPAF 252
Db 165 ECKIYSERVYDADWDADFCLPLAALMNQFLCVHGGLSPEINTLDDIRLDRFKPEPPAY 224

Qy 253 GPMCDLLWSDSEDFGNEKSOEHFHNVTVCGSFYFNPVPAVCEFLQNNLLSIIRAHEAQ 312
Db 225 GPMCDLLWSDLEDFGNEKTEQHEFHNVTVCGSFYFNPVPAVCEFLQNNLLSIIRAHEAQ 284

Qy 313 DAGYMYRKSQTTGPPSLITIFSAFNLYDVNNKAAVLKYNNVNNIQQFNCSPHYWLP 372
Db 285 DAGYMYRKSQTTGPPSLITIFSAFNLYDVNNKAAVLKYNNVNNIQQFNCSPHYWLP 344

Qy 373 NFMVDVFTWSLFPVGEKVETMLVNVLISICSDDELMTGEDQFDG-SAAARKKIIIRNKIRAI 431
Db 345 NFMVDVFTWSLFPVGEKVETMLVNVLISICSDDELMTGEDQFDG-SAAARKKIIIRNKIRAI 403

Qy 432 GKMARVFSVLRESESVLTGLTPTGMLPSGLVLAGGQTLOS 474
Db 404 GKMARVFSVLRESESVLTGLTPTGMLPSGLVLAGGQTLOS 446

RESULT 14
P2BA_RAT
ID P2BA_RAT STANDARD; PRT; 521 AA.
AC P63329; P12816; P20652;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)

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Db 240 RRLDRFKPPAFGPMCDLLWSDPSEDFGNEKSEQHFSHTVRCGSYFYNYPAVCEFLQNN 299
Qy 301 NLLSIIRAHEAQDAGYMYRKSQTGTGPPSLITIFSAAPNYLDVYNNKAALVLYENNVNIR 360
Db 300 NLLSIIRAHEAQDAGYMYRKSQTGTGPPSLITIFSAAPNYLDVYNNKAALVLYENNVNIR 359
Qy 361 QFNCSPPHYWLPNFMDFVFTWSLPPFVGEKVTMLVNVLSICSDDELMTEGEDQFDGSAAR 420
Db 360 QFNCSPPHYWLPNFMDFVFTWSLPPFVGEKVTMLVNVLSICSDDELMTEGEDQFDGSAAR 419
Qy 421 KEIIRNKIRAIGKMARVSVLRRESESVLTILKGLTPTGMLPSGVLGGRTQLQSGNDVMQ 480
Db 420 KEIIRNKIRAIGKMARVSVLRRESESVLTILKGLTPTGMLPSGVLGGRTQLQSGNDVMQ 479
Qy 481 LAVPQMDGTPHSPANNSHNACREFLFFSSCLSS 515
Db 480 LAVPQMDGTPHSPANNSHNACREFLFFSSCLSS 514

RESULT 2
B36222
phosphoprotein phosphatase (EC 3.1.3.16) 3-beta catalytic chain, splice form 2 - human
N;Alternate names: calcineurin catalytic chain; calcineurin chain A beta; calcineurin ch
C;Species: Homo sapiens (man)
C;Date: 04-Oct-1991 #sequence_revision 13-Jan-1993 #text_change 16-Aug-2004
C;Accession: B36222; S14272
R;Guerini, D.; Klee, C.B.
A;Title: Cloning of human calcineurin A: evidence for two isozymes and identification of
A;Reference number: A36222; MUID:90083232; PMID:2556704
A;Accession: B36222
A;Molecule type: mRNA
A;Residues: 1-524 <GUE>
A;Cross-references: UNIPROT:P16299; GB:M29551; NID:g180708; PIDN:AAA35706.1; PID:g180709
R;McPartlin, A.E.; Barker, H.M.; Cohen, P.T.W.
Biochim. Biophys. Acta 1088, 308-310, 1991
A;Title: Identification of a third alternatively spliced cDNA encoding the catalytic sub
A;Reference number: S14272; MUID:91159485; PMID:1848109
A;Accession: S14272
A;Molecule type: mRNA
A;Residues: 1-395, 'V', 396-456, 467-524 <MCP>
C;Genetics:
A;Gene: GDB:PPP3CB
A;Cross-references: GDB:I31362; OMIM:114106
A;Map position: 10q21-10q22
C;Complex: heterodimer with calcineurin regulatory chain
C;Function:
A;Description: catalyzes hydrolysis of peptidyl-phosphoserine or -phosphothreonine to re
C;Superfamily: Calcineurin catalytic chain; phosphoesterase core homology; phosphoprotei
C;Keywords: alternative splicing; heterodimer; iron; metalloprotein; phosphoprotein; pho
F;1-524/Product: protein phosphatase 3-beta catalytic chain splice form 2 #status predic
F;1-456,467-524/Product: protein phosphatase 3-beta catalytic chain splice form 3 #statu
F;65-337/Domain: phosphoprotein phosphatase homology <PPP>
F;93-161/Domain: phosphoesterase core homology <PSP>
F;93,161/Domain: phosphoesterase core homology <PSP>
F;93,161/Binding site: iron (Asp, His, Asp) #status predicted
F;127,159,208,290/Binding site: zinc (Asp, Asn, His, His) #status predicted
F;130,160,320/Active site: Asp, His, Tyr #status predicted
F;131,263/Binding site: substrate phosphate (Arg) #status predicted
F;420/Binding site: phosphate (Ser) (covalent) (by calmodulin-dependent kinase II) #stat

Qy 1 MAAPAPARAAPPPPPPPPPGADRVVKAVFPFPTHRLTSEVFDLGI PRVDVLKNHLV 60
Db 1 MAAPAPARAAPPPPPPPPPGADRVVKAVFPFPTHRLTSEVFDLGI PRVDVLKNHLV 60
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Db 61 KEGRVDEIARLIINEGAAILRREKTMIEVEAPITVCGDIHGQFFDLMKLFEVGGSPANT 120
Qy 121 RYFLGLGYVDRGYFSIEHVLGTEDISINPHNNINECVLYLWLKILYPSLTFLLLRGNHE 180
Db 121 RYFLGLGYVDRGYFSIEHVLGTEDISINPHNNINECVLYLWLKILYPSLTFLLLRGNHE 161

Qy 121 RYFLGLGYVDRGYFSIEHVLGTEDISINPHNNINECVLYLWLKILYPSLTFLLLRGNHE 180
Db 121 RYFLGLGYVDRGYFSIEHVLGTEDISINPHNNINECVLYLWLKILYPSLTFLLLRGNHE 161
Qy 181 CRHLTEYFTFKQCKIKYSERVYEAQWAFDSPLAALLNQQLFCLVHGGLSPEIHTLDDI 240
Db 162 CRHLTEYFTFKQCKIKYSERVYEAQWAFDSPLAALLNQQLFCLVHGGLSPEIHTLDDI 221
Qy 241 RRLDRFKPEPPAFGPMCDLLWSDPSEDFGNEKSEQHFSHTVRCGSYFYNYPAVCEFLQNN 300
Db 222 RRLDRFKPEPPAFGPMCDLLWSDPSEDFGNEKSEQHFSHTVRCGSYFYNYPAVCEFLQNN 281
Qy 301 NLLSIIRAHEAQDAGYMYRKSQTGTGPPSLITIFSAAPNYLDVYNNKAALVLYENNVNIR 360
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Db 342 QFNCSPPHYWLPNFMDFVFTWSLPPFVGEKVTMLVNVLSICSDDELMTEGEDQFDGSAAR 401
Qy 421 KEIIRNKIRAIGKMARVSVLRRESESVLTILKGLTPTGMLPSGVLGGRTQLQ 474
Db 402 KEIIRNKIRAIGKMARVSVLRRESESVLTILKGLTPTGMLPSGVLGGRTQLQ 455

RESULT 3
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phosphoprotein phosphatase (EC 3.1.3.16) 3-beta catalytic chain - rat
N;Alternate names: calcineurin catalytic chain; calcineurin chain A-beta; protein phosph
C;Species: Rattus norvegicus (Norway rat)
C;Date: 23-Mar-1990 #sequence_revision 23-Mar-1990 #text_change 16-Aug-2004
C;Accession: A33794; I36491
R;Kuno, T.; Takeda, T.; Hirai, M.; Ito, A.; Mukai, H.; Tanaka, C.
Biochem. Biophys. Res. Commun. 165, 1352-1358, 1989
A;Title: Evidence for a second isoform of the catalytic subunit of calmodulin-dependent
A;Reference number: A33794; MUID:90121248; PMID:2558657
A;Accession: A33794
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-525 <KUN>
A;Cross-references: UNIPROT:P20651; GB:M31809; NID:g203228; PIDN:AAA40848.1; PID:g203229
R;Madzinski, B.E.; Headley, L.E.; Johnson, G.L.
J. Biol. Chem. 265, 21504-21508, 1990
A;Title: Multiplicity of protein serine-threonine phosphatases in PC12 pheochromocytoma
A;Reference number: A36491; MUID:91072341; PMID:2174876
A;Accession: I36491
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 245-315 <WAD>
A;Cross-references: GB:M58441; NID:g206308; PIDN:AAA1915.1; PID:g206309; GB:J05720
C;Superfamily: Calcineurin catalytic chain; phosphoesterase core homology; phosphoprotei
C;Keywords: phosphoprotein; phosphoric monoester hydrolase
F;65-337/Domain: phosphoprotein phosphatase homology <PPP>
F;93-161/Domain: phosphoesterase core homology <PSP>
F;421/Binding site: phosphate (Ser) (covalent) (by calmodulin-dependent kinase II) #stat

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Qy 1 MAAPAPARAAPPPPPPPPPGADRVVKAVFPFPTHRLTSEVFDLGI PRVDVLKNHLV 60
Db 1 MAAPAPARAAPPPPPPPPPGADRVVKAVFPFPTHRLTSEVFDLGI PRVDVLKNHLV 60
Qy 61 KEGRVDEIARLIINEGAAILRREKTMIEVEAPITVCGDIHGQFFDLMKLFEVGGSPANT 120
Db 61 KEGRVDEIARLIINEGAAILRREKTMIEVEAPITVCGDIHGQFFDLMKLFEVGGSPANT 120
Qy 121 RYFLGLGYVDRGYFSIEHVLGTEDISINPHNNINECVLYLWLKILYPSLTFLLLRGNHE 180
Db 121 RYFLGLGYVDRGYFSIEHVLGTEDISINPHNNINECVLYLWLKILYPSLTFLLLRGNHE 161

Qy	181	CRHLTYFTFKQCKKIYKSRVYACMEAFDSFLAALLNQOFLCVHGGLSPEIHTLDDI	240
Db	162	CRHLTYFTFKQCKKIYKSRVYACMEAFDSFLAALLNQOFLCVHGGLSPEIHTLDDI	221
Qy	241	RLDRFKPEPPAFGPMCDLLWSDFSGNEKSQEHFSHTVRCGSYFYNYPAVCEFLQNN	300
Db	222	RLDRFKPEPPAFGPMCDLLWSDFSGNEKSQEHFSHTVRCGSYFYNYPAVCEFLQNN	281
Qy	301	NLLSIIIRAHEAQAGYRMYSKSTQTGPFSLITIFSAPNYLDVYNNKAAVLKYENNVNMR	360
Db	282	NLLSIIIRAHEAQAGYRMYSKSTQTGPFSLITIFSAPNYLDVYNNKAAVLKYENNVNMR	341
Qy	361	QNCSPHPYWLPNFMDVFTWSLFPVGSKVTMLVNVLSICSDDELMTEGEDQFD-GSAAA	419
Db	342	QNCSPHPYWLPNFMDVFTWSLFPVGSKVTMLVNVLSICSDDELMTEGEDQFDVGSAAA	401
Qy	420	RXEIIRNKIRAIGKMARVFSVLREESSVLTGLTPTGMLPSPGVLAGGRQTLOS	474
Db	402	RXEIIRNKIRAIGKMARVFSVLREESSVLTGLTPTGMLPSPGVLAGGRQTLOS	456
RESULT 4			
JT0976			
phosphoprotein phosphatase (EC 3.1.3.16) 3-alpha catalytic chain - mouse (fragment)			
N:Alternate names: calcineurin catalytic chain; calcineurin chain A; protein phosphatase			
C:Species: Mus musculus (house mouse)			
C>Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004			
C:Accession: JT0976; B45110			
R:Giiri, P.R.; Higuchi, S.; Kincaid, R.L.			
Biochem. Biophys. Res. Commun. 181, 252-258, 1991			
A:Title: Chromosomal mapping of the human genes for the calmodulin-dependent protein phosphatase			
A:Reference number: JT0976; MUID:92068200; PMID:1659808			
A:Accession: JT0976			
A:Molecule type: mRNA			
A:Residues: 1-515 <GIR>			
A:Cross-references: UNIPROT:P48453; GB:M81483; NID:g192537; PIDN:AAA37411.1; PID:g192538			
A:Experimental source: thymocyte			
R:Gaestel, M.; Benndorf, R.; Hayess, K.; Priemer, E.; Engel, K.			
J. Biol. Chem. 267, 21607-21611, 1992			
A:Title: Dephosphorylation of the small heat shock protein hsp25 by calcium/calmodulin-			
A:Reference number: A45110; MUID:93016109; PMID:1328240			
A:Accession: B45110			
A:Status: preliminary; not compared with conceptual translation			
A:Molecule type: nucleic acid			
A:Residues: 310-406 <GAE>			
A:Experimental source: Ehrlich ascites tumor cells			
A:Note: sequence extracted from NCBI backbone (NCBIP:116730)			
C:Comment: Multiple catalytic subunits of the Ca2+ and calmodulin (CaM)-dependent protein phosphatase			
C:Genetics:			
A:Map position: 10			
C:Superfamily: calcineurin catalytic chain; phosphoesterase core homology; phosphoprotein			
C:Keywords: calmodulin binding; phosphoprotein; phosphoric monoester hydrolase			
F:55-327/Domain: phosphoprotein phosphatase homology <PPP>			
F:83-151/Domain: phosphoesterase core homology <PEC>			
F:411/Binding site: phosphate (Ser) (covalent) (by calmodulin-dependent kinase II) #start			
Query Match 84.4%; Score 2321; DB 2; Length 515;			
Best Local Similarity 95.3%; Pred. No. 2.3e-170;			
Matches 443; Conservative 1; Mismatches 1; Indels 20; Gaps 3;			
Qy	11	PPPPPPPPPGADRVVKAVPFPPTHRLTSEVFDLGGIPRVDVLKNHLVKEGRVDEETA	70
Db	1	PPPPPPPPPLGADRVVKAVPFPPTHRLTSEVFDMDGIPRVDVLKNHLVKEGRVDEETA	60
Qy	71	LRIINEGAAILRREKTMIEVEAPITVCGDIHQGFQFDLMKLFVGGSSPANTRYLFLGDYVD	130
Db	61	LRIINEGAAILRREKTMIEVEAPITVCGDIHQGFQFDLMKLFVGGSSPANTRYLFLGDYVD	120
Qy	131	RGVFSFTEHLVGTSDISINPHNNINECVLYLWVILKILYPSSTFLLRGNHNECHRLTYFTFF	190
Db	121	RGVFSFTEHLVGTSDISINPHNNINECVLYLWVILKILYPSSTFLLRGNHNECHRLTYFTFF	161

Proc. Natl. Acad. Sci. U.S.A. 85, 8983-8987, 1988
A>Title: Characterization of a cDNA clone encoding the calmodulin-binding domain of mouse
A:Reference number: A31257; MUID:89057863; PMID:2848250
A:Accession: A31257
A:Molecule type: mRNA
A:Residues: 215-521 <X12>
A:Cross-references: GB:J04134; NID:g192656; PIDN:AAA37432.1; PID:g192657
A>Note: bovine calcineurin tryptic fragments were also sequenced
R:Gaestel, M.; Benndorf, R.; Hayess, K.; Priemer, E.; Engel, K.
J. Biol. Chem. 267, 21607-21611, 1992
A>Title: Dephosphorylation of the small heat shock protein hsp25 by calcium/calmodulin-d
A:Reference number: A45110; MUID:93016109; PMID:1328240
A:Accession: A45110
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 311-406 <GAE>
A:Experimental source: Ehrlich ascites tumor cells
A>Note: sequence extracted from NCB1 backbone (NCBIP:116727)
R:Fruman, D.A.; Pai, S.Y.; Burakoff, S.J.; Blierer, B.E.
Mol. Cell. Biol. 15, 3857-3863, 1995
A>Title: Characterization of a mutant calcineurin A alpha gene expressed by EL4 lymphoma
A:Reference number: I57562; MUID:953111985; PMID:7791792
A:Accession: I57562
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 467-476, 'N', 478-491 <RES>
A:Cross-references: GB:S78668; NID:g1042087; PIDN:AAB34675.1; PID:g1042088
A>Note: this mutation changes an evolutionarily conserved aspartic acid to asparagine wh
C:Superfamily: Calcineurin catalytic chain; phosphoesterase core homology; phosphoprotei
C:Keywords: calmodulin binding; phosphoprotein; phosphoric monoester hydrolase
F:156-328/Domain: phosphoprotein phosphatase homology <PPP>
F:184-152/Domain: phosphoesterase core homology <PEC>
F:391-414/Region: calmodulin binding #status predicted
F:411/Binding site: phosphate (Ser) (covalent) (by calmodulin-dependent kinase II) #stat

Query Match 74.7%; Score 2054.5; DB 2; Length 521;
Best Local Similarity 83.4%; Pred. No. 6.9e-150;
Matches 386; Conservative 35; Mismatches 21; Indels 21; Gaps 4;

QY 13 PPPPPPPGADRVVKA VFPFPTHRLTSEEVFDLDGIPRVDLVKNHLVKEGRVDEIARL 72
DB 4 PKADPKLSTTDRVVKA VFPFPPSHRLTAKEVFDNDGKPRVDILKAHLMKGRLEESVALR 63
QY 73 IINEGAAILRREKTMIEVEAPITVCGDIHGQFFDLMLKLFVGGSPANTRYILFLGDYVDRG 132
DB 64 IITEGASILRQEKNLDDIDAPVTVCGDTHGQFFDLMLKLFVGGSPANTRYILFLGDYVDRG 123
QY 133 YFSIEHVLGTEDISINPHNNINECVLYLWVLYKILYPTSLFLLLRGNHCHRLTEYFTPKQ 192
DB 124 YFSI-----ECVLYLWALKILYPKTLF--LLRGNHCHRLTEYFTPKQ 164
QY 193 ECKIKYSERVYEAQWAEAFDSLPLAALNQOFLCVHGGSLSPETHTLDDIRRLDRPKPEPAF 252
DB 165 ECKIKYSERVYDQWDAFDCPLAALMNQOFLCVHGGSLSPETHTLDDIRKLDRFKPEPAY 224
QY 253 GPMCDLLWSDPSDFGNEKSOEHFSHNTVRGCSYFYNYPAVCEFLQNNLLSIIRAHAQ 312
DB 225 GPMCDLLWSDPLEDFGNEKTQEHFTHTNVRGCSYFYSYPVAVCDFLQNNLLSIIRAHAQ 284
QY 313 DAGYMYRKSQTTGPPSLITIFSAAPNYLDVYNNKAAVLKYENNVNINIQFNCSPHPYWL 372
DB 285 DAGYMYRKSQTTGPPSLITIFSAAPNYLDVYNNKAAVLKYENNVNINIQFNCSPHPYWL 344
QY 373 NFMDFVFTWSLPFVGEKVTMELVNVLSICSDDELMTGEDQFDG--SAAARKEIIRNKIRAI 431
DB 345 NFMDFVFTWSLPFVGEKVTMELVNVNINICSDDELGSE--BDGFDGATAAARKEVIRNKIRAI 403
QY 432 GKMARVFSVLRSEESVLTLLKGLTPTGMLPSGVLAGGQRTLOS 474
DB 404 GKMARVFSVLRSEESVLTLLKGLTPTGMLPSGVLAGGQRTLOS 446

RESULT 8

A33264
phosphoprotein phosphatase (EC 3.1.3.16) 3-alpha catalytic chain - rat
N:Alternate names: calcineurin catalytic chain; calcineurin chain A-alpha; protein phosph
C:Species: Rattus norvegicus (Norway rat)
C>Date: 21-Feb-1990 #sequence revision 21-Feb-1990 #text_change 16-Aug-2004
C:Accession: A33264; S27349; H36491
R:Rito, A.; Hashimoto, T.; Hirai, M.; Takeda, T.; Shuntoh, H.; Kuno, T.; Tanaka, C.
Biochem. Biophys. Res. Commun. 163, 1492-1497, 1989
A>Title: The complete primary structure of calcineurin A, a calmodulin binding protein h
A:Reference number: A33264; MUID:89392066; PMID:2551293
A:Accession: A33264
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-521 <ITO>
A:Cross-references: UNIPROT:P20652; GB:M29275; NID:g203494; PIDN:AAA40940.1; PID:g203495
R:Chang, C.D.; Takeda, T.; Mukai, H.; Shuntoh, H.; Kuno, T.; Tanaka, C.
Biochem. J. 288, 801-805, 1992
A>Title: Molecular cloning and characterization of the promoter region of the calcineuri
A:Reference number: S27349; MUID:93111954; PMID:1335233
A:Accession: S27349
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-19 <CHA>
A:Cross-references: EMBL:D10480; NID:g220679; PIDN:BAA01283.1; PID:g220680
R:Wadzinski, B.E.; Heasley, L.E.; Johnson, G.L.
J. Biol. Chem. 265, 21504-21508, 1990
A>Title: Multiplicity of protein serine-threonine phosphatases in PC12 pheochromocytoma
A:Reference number: A36491; MUID:91072341; PMID:2174876
A:Accession: H36491
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 236-306 <WAD>
A:Cross-references: GB:M58440; NID:g206306; PIDN:AAA41914.1; PID:g206307; GB:J05720
C:Superfamily: Calcineurin catalytic chain; phosphoesterase core homology; phosphoprotei
C:Keywords: phosphoprotein; phosphoric monoester hydrolase
F:156-328/Domain: phosphoprotein phosphatase homology <PPP>
F:184-152/Domain: phosphoesterase core homology <PEC>
F:411/Binding site: phosphate (Ser) (covalent) (by calmodulin-dependent kinase II) #stat

Query Match 74.7%; Score 2054.5; DB 2; Length 521;
Best Local Similarity 83.4%; Pred. No. 6.9e-150;
Matches 386; Conservative 35; Mismatches 21; Indels 21; Gaps 4;

QY 13 PPPPPPPGADRVVKA VFPFPTHRLTSEEVFDLDGIPRVDLVKNHLVKEGRVDEIARL 72
DB 4 PKADPKLSTTDRVVKA VFPFPPSHRLTAKEVFDNDGKPRVDILKAHLMKGRLEESVALR 63
QY 73 IINEGAAILRREKTMIEVEAPITVCGDIHGQFFDLMLKLFVGGSPANTRYILFLGDYVDRG 132
DB 64 IITEGASILRQEKNLDDIDAPVTVCGDTHGQFFDLMLKLFVGGSPANTRYILFLGDYVDRG 123
QY 133 YFSIEHVLGTEDISINPHNNINECVLYLWVLYKILYPTSLFLLLRGNHCHRLTEYFTPKQ 192
DB 124 YFSI-----ECVLYLWALKILYPKTLF--LLRGNHCHRLTEYFTPKQ 164
QY 193 ECKIKYSERVYEAQWAEAFDSLPLAALNQOFLCVHGGSLSPETHTLDDIRRLDRPKPEPAF 252
DB 165 ECKIKYSERVYDQWDAFDCPLAALMNQOFLCVHGGSLSPETHTLDDIRKLDRFKPEPAY 224
QY 253 GPMCDLLWSDPSDFGNEKSOEHFSHNTVRGCSYFYNYPAVCEFLQNNLLSIIRAHAQ 312
DB 225 GPMCDLLWSDPLEDFGNEKTQEHFTHTNVRGCSYFYSYPVAVCDFLQNNLLSIIRAHAQ 284
QY 313 DAGYMYRKSQTTGPPSLITIFSAAPNYLDVYNNKAAVLKYENNVNINIQFNCSPHPYWL 372
DB 285 DAGYMYRKSQTTGPPSLITIFSAAPNYLDVYNNKAAVLKYENNVNINIQFNCSPHPYWL 344
QY 373 NFMDFVFTWSLPFVGEKVTMELVNVLSICSDDELMTGEDQFDG--SAAARKEIIRNKIRAI 431
DB 345 NFMDFVFTWSLPFVGEKVTMELVNVNINICSDDELGSE--BDGFDGATAAARKEVIRNKIRAI 403
QY 432 GKMARVFSVLRSEESVLTLLKGLTPTGMLPSGVLAGGQRTLOS 474

Db	404	GKMARVFSVLRESESVLTLLKGLTPTGMPLPSGVLSGGKQTLLQS	446
RESULT 9			
JC1283			
phosphoprotein phosphatase (EC 3.1.3.16) 3-gamma catalytic chain - human			
N;Alternate names: calcineurin catalytic chain; calcineurin chain A; protein phosphatase			
C;Species: Homo sapiens (man)			
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-2004			
C;Accession: JC1283			
R;Muramatsu, T.; Kincaid, R.L.			
Biochem. Biophys. Res. Commun. 188, 265-271, 1992			
A;Title: Molecular cloning and chromosomal mapping of the testis-spec			
A;Reference number: JC1283; MUID:93038669; PMID:1339277			
A;Accession: JC1283			
A;Molecule type: mRNA			
A;Residues: 1-502 <MUR>			
A;Cross-references: UNIPROT:P48454; GB:S46622; NID:g258000; PIDN:AAB23769.1; PID:g258001			
A;Experimental source: testis			
C;Genetics:			
A;Gene: GDB:PPP3CC			
A;Cross-references: GDB:I36027; OMIM:114107			
A;Map position: 8pter-8qter			
C;Complex: heterodimer with calcineurin regulatory chain			
C;Function:			
A;Description: catalyzes hydrolysis of peptidyl-phosphoserine or -phosphothreonine to re			
A;Note: this isoform is testis specific and is associated with sperm flagellar motility			
C;Superfamily: Calcineurin catalytic chain; phosphoesterase core homology; phosphoprotei			
C;Keywords: heterodimer; iron; metalloprotein; phosphoprotein; phosphoric monoester hyd			
F;52-324/Domain: phosphoprotein phosphatase homology <PPP>			
F;80-148/Domain: phosphoesterase core homology <PEC>			
F;86,88,114/Binding site: iron (Asp, His, Asp) #status predicted			
F;114,146,195,277/Binding site: zinc (Asp, Asn, His, His) #status predicted			
F;117,147,307/Active site: Asp, His, Tyr #status predicted			
F;118,250/Binding site: substrate phosphate (Arg) #status predicted			
F;405/Binding site: phosphate (Ser) (covalent) (by calmodulin-dependent kinase II) #stat			
Query Match 72.2%; Score 1985; DB 1; Length 502;			
Best Local Similarity 82.3%; Pred. No. 1.4e-144;			
Matches 371; Conservative 40; Mismatches 18; Indels 22; Gaps 4;			
Qy	24	DRVVKAVPPPTPRLTSEEVFDLGGIPRVVDVKNHVKEGRVDEIRALRINEGAAILRR	83
Db	12	DRVVKAVPPPTPRLTSEEVFDLGGIPRVVDVKNHVKEGRVDEIRALRINEGAAILRQ	70
Qy	84	EKTMIIEVAPITVCGDIHGQFPDLMKLFEVGGSPANTRYFLGDIYVDRGYFSIEHVLGTE	143
Db	71	EKTMIIEVAPITVCGDIHGQFPDLMKLFEVGGSPANTRYFLGDIYVDRGYFSI-----	123
Qy	144	DISINPHNNINECVLYMWLILYPSITFLLRGNHSECHLTETFTFKQECRIKYSERVY	203
Db	124	-----ECVLYLWSLKNHPKTLF--LLRGNHSECHLTETFTFKQECRIKYSQVY	171
Qy	204	EACMEAFDSIPLAALLNQOFLCVHGGSLSPETHTLDDIRLRDRKEPPAFGPMCDLLWSDP	263
Db	172	DACMETFDCLPLAALLNQOFLCVHGGSLSPETHTLDDIRLRDRKEPPAFGPMCDLLWSDP	231
Qy	264	SEDFGNKESQHFHSNTVRGCSYFYNYPAVCEFLQNNLLSIIIRAHEADAGYRMYSKQ	323
Db	232	LEDYGSSEKTLTETHTVTRGCSYFYNYPAVCEFLQNNLLSIIIRAHEADAGYRMYSKQ	291
Qy	324	TTGFPSSLITIFSPAPNYLDVYNNKAAVLKYENNVMNIRQFNCSPPHYLWLPNFMDFVFTW	383
Db	292	ATGFPSSLITIFSPAPNYLDVYNNKAAVLKYENNVMNIRQFNCSPPHYLWLPNFMDFVFTW	351
Qy	384	FVGEKVTMLVNVLSICSDDELMTGEDQFDGSAARKEIIRNKIRAIQKMARVFSVLRE	443
Db	352	SEDFGNKESQHFHSNTVRGCSYFYNYPAVCEFLQNNLLSIIIRAHEADAGYRMYSKQ	291
Qy	324	TTGFPSSLITIFSPAPNYLDVYNNKAAVLKYENNVMNIRQFNCSPPHYLWLPNFMDFVFTW	383
Db	292	ATGFPSSLITIFSPAPNYLDVYNNKAAVLKYENNVMNIRQFNCSPPHYLWLPNFMDFVFTW	351
Qy	384	FVGEKVTMLVNVLSICSDDELMTGEDQFDGSAARKEIIRNKIRAIQKMARVFSVLRE	443
Db	352	FVGEKVTMLVNVLSICSDDELMTGEDQFDGSAARKEIIRNKIRAIQKMARVFSVLRE	409
Qy	444	ESESVLTLLKGLTPTGMPLPSGVLSGGKQTLLQS	474
Db	410	ESESVLTLLKGLTPTGMPLPSGVLSGGKQTLLQS	440

RESULT 10			
A38193			
phosphoprotein phosphatase (EC 3.1.3.16) 3-gamma catalytic chain - mouse			
N;Alternate names: calcineurin catalytic chain; calcineurin chain A; nonneural calmoduli			
C;Species: Mus musculus (house mouse)			
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 16-Aug-2004			
C;Accession: A38193			
R;Muramatsu, T.; Giri, P.R.; Higuchi, S.; Kincaid, R.L.			
Proc. Natl. Acad. Sci. U.S.A. 89, 529-533, 1992			
A;Title: Molecular cloning of a calmodulin-dependent phosphatase from murine testis: ide			
A;Reference number: A38193; MUID:92115694; PMID:1309945			
A;Accession: A38193			
A;Status: preliminary			
A;Molecule type: mRNA			
A;Residues: 1-513 <MUR>			
A;Cross-references: UNIPROT:P48455; GB:M81475; NID:g200465; PIDN:AAA39968.1; PID:g200466			
A;Experimental source: testis			
A;Note: sequence extracted from NCBI backbone (NCBIN:75959, NCBI:P:75960)			
C;Function:			
A;Description: catalyzes the hydrolysis of peptidyl-phosphoserine and -phosphothreonine			
A;Note: this isoform is testis specific and is associated with sperm flagellar motility			
C;Superfamily: Calcineurin catalytic chain; phosphoesterase core homology; phosphoprotei			
C;Keywords: calmodulin binding; phosphoric monoester hydrolase; testis			
F;52-324/Domain: phosphoprotein phosphatase homology <PPP>			
F;80-148/Domain: phosphoesterase core homology <PEC>			
Query Match 69.8%; Score 1919.5; DB 2; Length 513;			
Best Local Similarity 78.9%; Pred. No. 1.6e-139;			
Matches 356; Conservative 47; Mismatches 25; Indels 23; Gaps 4;			
Qy	24	DRVVKAVPPPTPRLTSEEVFDLGGIPRVVDVKNHVKEGRVDEIRALRINEGAAILRR	83
Db	12	ERVVKAVPPPTPRLTSEEVFDLGGIPRVVDVKNHVKEGRVDEIRALRINEGAAILRQ	70
Qy	84	EKTMIIEVAPITVCGDIHGQFPDLMKLFEVGGSPANTRYFLGDIYVDRGYFSIEHVLGTE	143
Db	71	EKTMIIEVAPITVCGDIHGQFPDLMKLFEVGGSPANTRYFLGDIYVDRGYFSI-----	123
Qy	144	DISINPHNNINECVLYMWLILYPSITFLLRGNHSECHLTETFTFKQECRIKYSERVY	203
Db	124	-----ECVLYLWSLKNHPKTLF--LLRGNHSECHLTETFTFKQECRIKYSERVY	171
Qy	204	EACMEAFDSIPLAALLNQOFLCVHGGSLSPETHTLDDIRLRDRKEPPAFGPMCDLLWSDP	263
Db	172	DACMETFDCLPLAALLNQOFLCVHGGSLSPETHTLDDIRLRDRKEPPAFGPMCDLLWSDP	231
Qy	264	SEDFGNKESQHFHSNTVRGCSYFYNYPAVCEFLQNNLLSIIIRAHEADAGYRMYSKQ	323
Db	232	LEDYGSSEKTLTETHTVTRGCSYFYNYPAVCEFLQNNLLSIIIRAHEADAGYRMYSKQ	291
Qy	324	TTGFPSSLITIFSPAPNYLDVYNNKAAVLKYENNVMNIRQFNCSPPHYLWLPNFMDFVFTW	383
Db	292	ATGFPSSLITIFSPAPNYLDVYNNKAAVLKYENNVMNIRQFNCSPPHYLWLPNFMDFVFTW	351
Qy	384	FVGEKVTMLVNVLSICSDDELMTGEDQFDGSAARKEIIRNKIRAIQKMARVFSVLRE	443
Db	352	FVGEKVTMLVNVLSICSDDELMTGEDQFDGSAARKEIIRNKIRAIQKMARVFSVLRE	408
Qy	444	ESESVLTLLKGLTPTGMPLPSGVLSGGKQTLLQS	474
Db	409	ESESVLTLLKGLTPTGMPLPSGVLSGGKQTLLQS	439
RESULT 11			
JC7241			
phosphoprotein phosphatase (EC 3.1.3.16), calcineurin catalytic chain [similarity] - sca			
N;Alternate names: Ca2+/calmodulin-dependent phosphoprotein phosphatase catalytic subunit			
C;Species: Patinopecten yessoensis (Yesso scallop)			
C;Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 16-Aug-2004			
C;Accession: JC7241; PC7069			
R;Uryu, M.; Nakatomi, A.; Watanabe, M.; Hatause, R.; Yazawa, M.			
J. Biochem. 127, 739-746, 2000			

A>Title: Molecular cloning of cDNA encoding two subunits of calcineurin from scallop testis

A:Reference number: JC7241

A:Accession: JC7241

A:Molecule type: mRNA

A:Residues: 1-486 <URY>

A:Cross-references: UNIPROT:Q9NWK8; DDBJ:AB041523

A:Experimental source: testis

A:Accession: PC7069

A:Molecule type: protein

A:Residues: 43-62;72-92;113-153;165-185;210-230;239-249;289-309;319-339;356-373;405-424

C:Comment: This testis-specific isoform functions during the maturation process. It is identical to the testis-specific isoform of calcineurin AII from scallop testis.

C:Genetics:

A:Gene: cna

C:function:

A:Description: catalyzes hydrolysis of peptidyl-phosphoserine or -phosphothreonine to release phosphate

C:Superfamily: Calcineurin catalytic chain; phosphoesterase core homology; phosphoprotein

C:Keywords: calmodulin binding; flagellar rotation; iron; metalloprotein; phosphoprotein

F:52-324/Domain: phosphoprotein phosphatase homology <PPP>

F:80-148/Domain: phosphoesterase core homology <P>

F:86,88,114/Binding site: Iron (Asp, His, Asp) #status predicted

F:114,146,195,277/Binding site: Zinc (Asp, Asn, His, His) #status predicted

F:117,147,307/Active site: Asp, His, Tyr #status predicted

F:118,250/Binding site: substrate phosphate (Arg) #status predicted

F:411/Binding site: phosphate (Thr) (covalent) (by calmodulin-dependent kinase II) #status predicted

Query Match 69.5%; Score 1910; DB 1; Length 486;

Best Local Similarity 73.3%; Pred. No. 7.8e-139;

Matches 363; Conservative 46; Mismatches 50; Indels 36; Gaps 6;

QY	24	DRVVKAVPPPT	HRLTSEVF	FDLDGIP	RDVVL	KHVLK	EGRVDE	IAIRINE	GAAILRR	83	
DB					:	:	:	:			
QY	11	ERVVKAPPP	SHKLNLSE	VFGV	GKPKPE	VYLKQH	FLTEGR	VTEDVAL	RIINDGA	MLRQ 70	
DB					:	:	:	:			
QY	84	EKTMIEVEAP	ITVCGD	IHGQFF	FDLMKL	FEVGS	PANTRY	FLGDV	VDRGYFS	IEHVLTGE 143	
DB					:	:	:	:			
QY	71	EKTMIEIEAP	TVCGD	IHGQFY	DLMLK	FEVGGT	PATTRY	FLGDV	VDRGYFSI	----- 123	
DB					:	:	:	:			
QY	144	DISINPHNN	INECVLYL	WLVLK	ILYPST	FLLLR	GNHECR	HLTEY	FTFKQEC	KIKYSERY 203	
DB					:	:	:	:			
QY	124	-----	ECVLYL	WLSKLL	HPNT	-FFML	RGNHECR	HLTEY	FTFKQEC	KIKYTERVY 171	
DB					:	:	:	:			
QY	204	EAGNEAFDS	LPLAALL	NOQFL	CVHGG	LSPEI	HTLDD	IRRLDR	FKPEPP	AFGPMCDLLWSDP 263	
DB					:	:	:	:			
QY	172	DAGMDAFDC	LPALAMN	QQFL	CVHGG	LSPEI	HTLED	IRKLD	RFKPEPP	AFGPMCDLLWSDP 231	
DB					:	:	:	:			
QY	264	SDDFGNKSE	QHEP	SHNTVR	CSFYNY	PAVCEP	LQNNLL	SIIRA	HAQAQD	AGYMYRSQ 323	
DB					:	:	:	:			
QY	232	LEDFGTEKT	SEHT	THNSVR	CSFYNY	AAACD	FLSQNNLL	SIIRA	HAQAQD	AGYMYRSQ 291	
DB					:	:	:	:			
QY	324	TTGFP	SLITIFS	PANLYD	VYNNK	AAVLK	YENNVN	NIQF	NCSPHY	MLPNFMDVFTWSLP 383	
DB					:	:	:	:			
QY	292	TTGFP	SLITIFS	PANLYD	VYNNK	AAVLK	YENNVN	NIQF	NCSPHY	MLPNFMDVFTWSLP 351	
DB					:	:	:	:			
QY	384	FVGEKTE	MLVNVL	STCSD	DELMT	-EGED	QFDGS	---AA	AKETIR	KNKIRAIGKQMARVPS 439	
DB					:	:	:	:			
QY	352	FVGEKTE	MLVNVL	STCSD	NELTA	EEEEEB	DGSDG	AAASR	KEVIK	KNKIRAIGKQMARVFT 411	
DB					:	:	:	:			
QY	440	VLREES	SVLT	TLKGL	PTGML	PSG	VL	AGGR	QTLQ	-----SCNDV	NQLAVPQWD 487
DB					:	:	:	:			
QY	412	VLREES	SVLT	QKGL	PTGML	PSG	VL	AGGR	QTLQ	-----SCNDV	NQLAVPQWD 487
DB					:	:	:	:			
QY	488	WGTP	PSFA	-NN	SHNA	501					
DB					:	:	:	:			
QY	472	RMP	PRKDA	VNN	SHKS	486					
DB					:	:	:	:			

RESULT 12

S70554

C:Species: Drosophila melanogaster

C:Date: 19-Mar-1998 #sequence revision 17-Apr-1998 #text_change 16-Aug-2004

C:Accession: S70554

R:Hong, C.S.; Ganetzky, B.

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 26, 2005, 14:04:18 ; Search time 58.073 Seconds
(without alignments)
1132.183 Million cell updates/sec

Title: US-09-435-257D-35
Perfect score: 875
Sequence: 1 MGNEASYPLEMCSHFDADEI.....BEFCVAVGGLDIHKRMVVDV 170

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	875	100.0	170	2	Aaw64200 Human cal
2	875	100.0	170	3	Aab09978 Human HCN
3	875	100.0	170	8	ADI27357 Human cal
4	870	99.4	169	7	Ades5926 Rat Prote
5	870	99.4	169	7	Ades5928 Human Pro
6	767	87.7	170	4	ABb60493 Drosophil
7	739	84.5	162	4	ABb65554 Drosophil
8	738	84.3	170	4	AAO14411 Calcineur
9	738	84.3	173	4	ABa64410 Amino aci
10	738	84.3	173	6	ADA55632 Human pro
11	738	84.3	187	4	AAU87327 Novel cen
12	738	84.3	187	8	ADI54642 Novel hum
13	738	84.3	189	4	AAm95239 Human rep
14	738	84.3	189	4	AAm43639 Human pol
15	738	84.3	189	4	AAm43564 Human pol
16	738	84.3	189	4	AAU19951 Novel hum
17	738	84.3	189	4	ABb95936 Human tes
18	738	84.3	189	4	AAU87615 Novel cen
19	738	84.3	189	8	ADI54930 Novel hum
20	738	84.3	189	8	Adm24660 Human PRO
21	738	84.3	189	8	Adm24585 Human PRO
22	733	83.8	170	3	ABb09977 Human CNB
23	501	57.3	197	8	ADS24073 Bacterial
24	496	56.7	175	2	AAy00881 Calcineur
25	496	56.7	175	8	ADS43790 Bacterial

26	429.5	49.1	195	8	ADS44352 Bacterial
27	429	49.0	185	8	ADN21422 Bacterial
28	398	45.5	90	3	AAG02990 Human eec
29	373.5	42.7	178	3	AAV77951 A. thalia
30	340.5	38.9	195	6	ABg74662 Murine ca
31	337.5	38.6	194	6	ABg74856 Human cal
32	337.5	38.6	194	7	ADD46021 Human Pro
33	337.5	38.6	194	7	ADE59921 Human Pro
34	337.5	38.6	194	7	ADb61228 Human Pro
35	337.5	38.6	194	7	ADE59917 Human Pro
36	337.5	38.6	195	6	ABg74661 Human Ca2
37	337.5	38.6	195	6	ABu89717 Protein d
38	323.5	37.0	189	4	ABb58936 Drosophil
39	316.5	36.2	213	8	ADN23634 Bacterial
40	308.5	35.3	195	8	ADN23801 Bacterial
41	292	33.4	196	4	AAW78527 Human Pro
42	292	33.4	196	6	ABg74656 Human Ca2
43	292	33.4	196	8	ADN04220 Antipsoxi
44	292	33.4	196	8	ABO84928 Human can
45	292	33.4	196	8	ADS85016 Human ato

ALIGNMENTS

RESULT 1
AAW64200
ID AAW64200 standard; protein; 170 AA.
XX
AC AAW64200;
XX
DT 09-NOV-1998 (first entry)
XX Human calcineurin.
DE
XX
KW Calcineurin; interferon receptor 1 binding protein; IR1B1; human.
XX Homo sapiens.
XX
XX WO9831796-A1.
XX
XX 23-JUL-1998.
XX
XX 15-JAN-1998; 98WO-US0000671.
XX
XX 15-JAN-1997; 97US-0035636P.
XX (YEDA) YEDA RES & DEV CO LTD.
XX (MCIN/) MCINNIS P A.
XX
XX Revel M, Abramovitch C, Chebath JE;
XX
XX WPI; 1998-414096/35.
XX
XX New isolated interferon receptor binding proteins - used to develop products for modulating sensitivity to interferon, e.g. in the treatment of tumours or for prolonging graft survival.
XX
XX Example 2; Page 35-36; 64pp; English.
XX
XX This polypeptide comprises the human calcium-binding protein, calcineurin -beta. A novel interferon receptor binding protein, IR1B1 (see AAW64199), of the invention shows marked homology, e.g. calcium binding sites (E-P handles), to calcineurin-beta; amino acid residues 50-171 show 59.8% similarity and 32.5% identity. IR1B1 polypeptides and polynucleotides can be used to develop products for modulating sensitivity to interferon, e.g. in cancer therapy and for prolonging graft survival
XX
XX Sequence 170 AA;

Query Match 100.0%; Score 875; DB 2; Length 170;
Best Local Similarity 100.0%; Pred. No. 2.8e-83;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 MGNEASYPLEMCSHFDADEIKRLGKRFKKLDLDSGSLSVSEEFMSLPQLQNPVLRVID 60
Db |||||
QY 1 MGNEASYPLEMCSHFDADEIKRLGKRFKKLDLDSGSLSVSEEFMSLPQLQNPVLRVID 60
Db |||||
QY 61 IFDTDGNGEVDKFEFIEGVVSQFSVKGDKQKLRFAFRFYDMKDGYISNGELFOVLKMMV 120
Db |||||
QY 61 IFDTDGNGEVDKFEFIEGVVSQFSVKGDKQKLRFAFRFYDMKDGYISNGELFOVLKMMV 120
Db |||||
QY 121 GNNLKDTQLQIQIVDKTIINADKGDGRISPFEEFCVAVGGGLDIHKMMVVDV 170
Db |||||
121 GNNLKDTQLQIQIVDKTIINADKGDGRISPFEEFCVAVGGGLDIHKMMVVDV 170
Db |||||

RESULT 2
AAB09978
ID AAB09978 standard; protein; 170 AA.
XX
AC AAB09978;
XX
DT 19-OCT-2000 (first entry)
XX
DE Human HCNB protein.
XX
KW Human; CNBII; calcineurin B; regulatory subunit; HCNB.
XX
OS Homo sapiens.
XX
PN CN1249347-A.
XX
PD 05-APR-2000.
XX
PF 30-SEP-1998; 98CN-00121923.
XX
PR 30-SEP-1998; 98CN-00121923.
XX
PA (UYFU-) UNIV FUDAN.
XX
PI Yu L, Zhang H, Zhao Y;
XX
WPI; 2000-400725/35.
XX
Preparation of human calcineurin regulatory subunit and its coding
PT sequence.
XX
PS Disclosure; Fig 1; 18pp; Chinese.
XX
This invention describes the novel coding sequence of CNBII, a new member
CC of the human Calcineurin (CN) regulatory subunit Calcineurin B (CNB)
CC family. The polypeptide coded by said sequence is the homolog of human
CC CNB gene. The process relates to the polypeptide coded by the
CC polynucleotide, and the application and preparing process of said
CC polynucleotide and said polypeptide. This sequence represents the human
CC HCNB protein described in the method of the invention
XX
SQ Sequence 170 AA;
Query Match 100.0%; Score 875; DB 3; Length 170;
Best Local Similarity 100.0%; Pred. No. 2.8e-83;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGNEASYPLEMCSHFDADEIKRLGKRFKKLDLDSGSLSVSEEFMSLPQLQNPVLRVID 60
Db |||||
QY 1 MGNEASYPLEMCSHFDADEIKRLGKRFKKLDLDSGSLSVSEEFMSLPQLQNPVLRVID 60
Db |||||
QY 61 IFDTDGNGEVDKFEFIEGVVSQFSVKGDKQKLRFAFRFYDMKDGYISNGELFOVLKMMV 120
Db |||||
QY 61 IFDTDGNGEVDKFEFIEGVVSQFSVKGDKQKLRFAFRFYDMKDGYISNGELFOVLKMMV 120
Db |||||
QY 121 GNNLKDTQLQIQIVDKTIINADKGDGRISPFEEFCVAVGGGLDIHKMMVVDV 170
Db |||||
121 GNNLKDTQLQIQIVDKTIINADKGDGRISPFEEFCVAVGGGLDIHKMMVVDV 170
Db |||||
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RESULT 3
ADI27357
ID ADI27357 standard; protein; 170 AA.
XX
AC ADI27357;
XX
DT 22-APR-2004 (first entry)
XX
Human calcineurin regulatory subunit B, PPP3R1.
XX
Antisense; enzyme; calcineurin; regulatory subunit B; PPP3R1;
KW immunosuppressive; nootropic; neuroprotective; protein phosphatase 3;
KW autoimmune disorder; aberrant calcium signaling; neurological disease;
KW Alzheimer's disease; human; gene.
XX
OS Homo sapiens.
XX
PN US2003236206-A1.
XX
PD 25-DEC-2003.
XX
PF 20-JUN-2002; 2002US-00177573.
XX
PR 20-JUN-2002; 2002US-00177573.
XX
PA (ISIS-) ISIS PHARM INC.
XX
Freier SM;
XX
WPI; 2004-070608/07.
XX
N-PSDB; ADI27256.
XX
New antisense oligonucleotide compounds, useful for diagnosing,
PT preventing and/or treating conditions with aberrant activity of PPP3R1,
PT such as autoimmune disorders, aberrant calcium signaling and Alzheimer's
PT disease.
XX
Disclosure; Page 31; 49pp; English.
XX
The invention relates to a new compound comprising 8-50 nucleobases in
CC length targeted to a nucleic acid molecule encoding protein phosphatase 3
CC (PPP3R1, the regulatory subunit of calcineurin), where the compound
CC specifically hybridizes with the nucleic acid and inhibits the expression
CC of PPP3R1, i.e. is an antisense oligonucleotide (AO). Also included are a
CC compound 8-50 nucleobases in length which specifically hybridizes with at
CC least an 8-nucleobase portion of an active site on a nucleic acid
CC molecule encoding PPP3R1, a method of inhibiting the expression of PPP3R1
CC in cells or tissues (comprising contacting the cells or tissues with AO
CC so that expression of PPP3R1 is inhibited), a method of treating an
CC animal having a disease or condition associated with PPP3R1 (comprising
CC administering AO to the animal so that expression of PPP3R1 is inhibited)
CC and a method of screening for an antisense compound (comprising
CC contacting a preferred target region of a nucleic acid molecule encoding
CC PPP3R1 with one or more candidate antisense compounds having at least an
CC 8-nucleobase portion which is complementary to the preferred target
CC region, and selecting for one or more candidate antisense compounds which
CC inhibit the expression of a nucleic acid encoding PPP3R1). The methods
CC and compositions of the present invention are useful for the diagnosis,
CC prevention and/or treatment of diseases or conditions associated with
CC aberrant expression or activity of PPP3R1, such as autoimmune disorders,
CC conditions having aberrant calcium signaling and neurological diseases,
CC like Alzheimer's disease. The present sequence is the PPP3R1 protein
CC sequence.
XX
SQ Sequence 170 AA;
Query Match 100.0%; Score 875; DB 8; Length 170;
Best Local Similarity 100.0%; Pred. No. 2.8e-83;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGNEASYPLEMCSHFDADEIKRLGKRFKKLDLDSGSLSVSEEFMSLPQLQNPVLRVID 60
|||
```

Db 1 MNEASYPLEMCSHFDADDEIKRLGRFKKLDLDNSGSLSVVEFMSLPELQQNPLVQRVID 60
Qy 61 IFDTDNGEVDPFKEFIEGVQSFSVKGDEQKLRFAFRIYDMDKGYISNGELFQVLKMWV 120
Db 61 IFDTDNGEVDPFKEFIEGVQSFSVKGDEQKLRFAFRIYDMDKGYISNGELFQVLKMWV 120
Qy 121 GNNLKDQTOLQIIVDKTIINADKDGGRISFBEFCVAVGGLDIHKMWVDV 170
Db 121 GNNLKDQTOLQIIVDKTIINADKDGGRISFBEFCVAVGGLDIHKMWVDV 170

RESULT 4
ADES5926
ID ADE55926 standard; protein; 169 AA.
XX
AC ADE55926;
XX
DT 29-JAN-2004 (first entry)
XX
DE Rat Protein P06705, SEQ ID NO 1760.
XX
KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
XX
OS Rattus norvegicus.
XX
PN WO2003016475-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
FA (GHEO) GEN HOSPITAL CORP.
FA (FARB) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX
DR WPI; 2003-268312/26.
DR GENBANK; P06705.
XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
PS Claim 1; Page; 1017pp; English.

XX The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a rat protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:

CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 169 AA;

Query Match 99.4%; Score 870; DB 7; Length 169;
Best Local Similarity 100.0%; Pred. No. 9.2e-83;
Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 GNEASYPLEMCSHFDADDEIKRLGRFKKLDLDNSGSLSVVEFMSLPELQQNPLVQRVID 61
Db 1 GNEASYPLEMCSHFDADDEIKRLGRFKKLDLDNSGSLSVVEFMSLPELQQNPLVQRVID 60
Qy 62 FDTDNGEVDPFKEFIEGVQSFSVKGDEQKLRFAFRIYDMDKGYISNGELFQVLKMWV 121
Db 61 FDTDNGEVDPFKEFIEGVQSFSVKGDEQKLRFAFRIYDMDKGYISNGELFQVLKMWV 120
Qy 122 NNLKDTOLQIIVDKTIINADKDGGRISFBEFCVAVGGLDIHKMWVDV 170
Db 121 NNLKDTOLQIIVDKTIINADKDGGRISFBEFCVAVGGLDIHKMWVDV 169

RESULT 5
ADES5928
ID ADE55928 standard; protein; 169 AA.
XX
AC ADE55928;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human Protein P06705, SEQ ID NO 1762.
XX
KW Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.
XX
OS Homo sapiens.
XX
PN WO2003016475-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
FA (GHEO) GEN HOSPITAL CORP.
FA (FARB) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX
DR WPI; 2003-268312/26.
DR GENBANK; P06705.
XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
PS Claim 1; Page; 1017pp; English.

XX The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially

expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene therapy). The sequence presented is a human protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

Query Match 99.4%; Score 870; DB 7; Length 169;
Best Local Similarity 100.0%; Pred. No. 9.2e-83;
Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 GNEASYPLEMCSHFDADEIKRLGKRFKLDLNSGSLSVVEFMSLPQLQNPVQVRVIDI 61
DB 1 GNEASYPLEMCSHFDADEIKRLGKRFKLDLNSGSLSVVEFMSLPQLQNPVQVRVIDI 60
QY 62 FDTGNGEVDPKFIEGVQSVKDGKEQKLRFAFRFYDMDKGYISNGELFQVLKMWVG 121
DB 61 FDTGNGEVDPKFIEGVQSVKDGKEQKLRFAFRFYDMDKGYISNGELFQVLKMWVG 120
QY 122 NNLKDTOLQOIYDKTIINADKDGGRISPEEFCAVVGGLDIHKMWVDV 170
DB 121 NNLKDTOLQOIYDKTIINADKDGGRISPEEFCAVVGGLDIHKMWVDV 169

RESULT 6
ABB60493
ID ABB60493 standard; protein; 170 AA.
XX AC ABB60493;
XX DT 26-MAR-2002 (first entry)
XX DE Drosophila melanogaster polypeptide SEQ ID NO 8271.
XX KW Drosophila; developmental biology; cell signalling; insecticide;
XX OS pharmaceutical.
XX OS Drosophila melanogaster.
XX PN WO200171042-A2.
XX PD 27-SEP-2001.
XX PF 23-MAR-2001; 2001WO-US009231.
XX PR 23-MAR-2000; 2000US-0191637P.
XX PR 11-JUL-2000; 2000US-00614150.
XX PA (PEKE) PE CORP NY.
XX PI Venter JC, Adams M, Li PWD, Myers EW;
XX DR WPI; 2001-656860/75.
XX DR N-PSDB; ABL04596.

The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

Query Match 87.7%; Score 767; DB 4; Length 170;
Best Local Similarity 85.9%; Pred. No. 5.7e-72;
Matches 146; Conservative 13; Mismatches 11; Indels 0; Gaps 0;
QY 1 MGNEASYPLEMCSHFDADEIKRLGKRFKLDLNSGSLSVVEFMSLPQLQNPVQVRVID 60
DB 1 MGNETSLPMDMCSNFDADAERRLGKRFKLDLNSGALSIDEFMSLPQLQNPVQVRVID 60
QY 61 IFDTGNGEVDPKFIEGVQSVKDGKEQKLRFAFRFYDMDKGYISNGELFQVLKMWV 120
DB 61 IFDADGNGEVDPKFIEGVQSVKDGKEQKLRFAFRFYDMDKGYISNGELFQVLKMWV 120
QY 121 GNNLKDTOLQOIYDKTIINADKDGGRISPEEFCAVVGGLDIHKMWVDV 170
DB 121 GNNLKDTOLQOIYDKTIICFADKDEKISPFDFCSVVGNTDIHKMWVDV 170

RESULT 7
ABB65554
ID ABB65554 standard; protein; 162 AA.
XX AC ABB65554;
XX DT 26-MAR-2002 (first entry)
XX DE Drosophila melanogaster polypeptide SEQ ID NO 23454.
XX KW Drosophila; developmental biology; cell signalling; insecticide;
XX OS pharmaceutical.
XX OS Drosophila melanogaster.
XX PN WO200171042-A2.
XX PD 27-SEP-2001.
XX PF 23-MAR-2001; 2001WO-US009231.
XX PR 23-MAR-2000; 2000US-0191637P.
XX PR 11-JUL-2000; 2000US-00614150.
XX PA (PEKE) PE CORP NY.
XX PI Venter JC, Adams M, Li PWD, Myers EW;
XX DR WPI; 2001-656860/75.
XX DR N-PSDB; ABL09657.

New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions.

Disclosure; SEQ ID NO 23454; 21pp + Sequence Listing; English.

The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA

CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
 CC ABB72072). The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 XX
 SQ Sequence 162 AA;

Query Match 84.5%; Score 739; DB 4; Length 162;
 Best Local Similarity 88.3%; Pred. No. 4.6e-69;
 Matches 143; Conservative 10; Mismatches 9; Indels 0; Gaps 0;

Qy 9 LEMCSHPADDEIKRLGKFKKLDLNSGSLSVSEFMSLPQLQNPVORVIDIFDTGNG 68
 Db 1 MEMCSNFADDEIRRLGKFKKLDLNSGSLSVSEFMSLPQLQNPVORVIDIFDADGNG 60

Qy 69 EVDFKEFTIEGVSQFSVKGDKQKLRFAFRIYDMDKDGYISNGELFQVLKMMVGNLKDQTQ 128
 Db 61 EVDFKEFTIQVSGFSVKGDKSLKLRFAFRIYDMNDGYSNGELFQVLKMMVGNLKDQTQ 120

Qy 129 LQIVDKTIINADKDGGRISPEFCFCAVVGGLDIHKMMVVDV 170
 Db 121 LQIVDKTIIGFADKDEGKISFDEFCFCAVVGNTDIHKMMVVDV 162

RESULT 8
 AA014411
 ID AA014411 standard; protein; 170 AA.
 AC AA014411;
 XX
 DT 07-MAY-2002 (first entry)
 XX
 DE Calceineurin B subunit beta protein.
 XX
 KW Calceineurin B subunit beta; Ca(2+)-binding regulatory subunit; agonist;
 KW antagonist; acute; chronic cardiac failure; arrhythmia; myocarditis;
 KW myocardial infarction; cardiac hypertrophy; cardiotoxicity; cardiac;
 KW chromosome localisation study; pulmonary hypertension; contraceptive;
 KW coronary heart disease; membrane bound soluble receptor; immunological;
 KW diagnostic reagent; tissue expression; antiarrhythmic; antiinflammatory;
 KW hypotensive; vaccine; gene therapy.
 XX
 OS Homo sapiens.
 XX
 FN WO200172772-A2.
 XX
 PD 04-OCT-2001;
 XX
 PF 28-MAR-2001; 2001WO-EP003528.
 XX
 PR 30-MAR-2000; 2000EP-00106093.
 XX
 PA (MERE) MERCK PATENT GMBH.
 XX
 FI Wilm C;
 XX
 PI WPI; 2001-616465/71.
 DR N-PSDB; AAK98734.
 XX
 XX Novel calcineurin B subunit beta polypeptides, for treating cardiac
 PT failure, myocardial infarction, cardiac hypertrophy, arrhythmia,
 PT myocarditis, pulmonary hypertension, cardiotoxicity and coronary heart
 PT disease.
 XX
 PS Claim 1; Page 34; 34pp; English.
 XX
 CC This sequence is the protein of a Calcineurin B subunit beta of the
 CC invention. The invention relates to newly identified Ca(2+)-binding
 CC regulatory subunit polypeptides and their encoding polynucleotides.
 CC referred to as "calcineurin B subunit beta", for use in diagnosis and
 CC identifying compounds that may be agonists, antagonists that are
 CC potentially useful in therapy, and to production of such polypeptides and
 CC polynucleotides. The polynucleotides and polypeptides of the invention

CC are useful for treating acute and chronic cardiac failure of different
 CC etiologies, myocardial infarction, cardiac hypertrophy, arrhythmia,
 CC myocarditis, pulmonary hypertension, cardiotoxicity, coronary heart
 CC disease, and as contraceptives. The polypeptides are also useful for
 CC identifying membrane bound soluble receptors. The polynucleotides are
 CC useful as a diagnostic reagent, for chromosome localisation studies, and
 CC for tissue expression studies. The polypeptides and polynucleotides are
 CC also useful as vaccines for inducing an immunological response in
 CC mammals. The polypeptides and polynucleotides of the invention are also
 CC useful for configuring screening methods for detecting the effect of
 CC added compounds on the production of mRNA and polypeptide in cells. The
 CC polypeptides and polynucleotides of the invention have cardiant,
 CC antiarrhythmic, antiinflammatory, hypotensive, and contraceptive
 CC activities, and can treat disorders by way of gene therapy
 XX
 SQ Sequence 170 AA;

Query Match 84.3%; Score 738; DB 4; Length 170;
 Best Local Similarity 84.7%; Pred. No. 6.2e-69;
 Matches 144; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

Qy 1 MGNEASYPLEMCSHPDADDEIKRLGKFKKLDLNSGSLSVSEFMSLPQLQNPVORVID 60
 Db 1 MGNEASYPAEMCSHPDNDDEIKRLGRRFKKLDLNSGSLSVSEFMSLPRLRNPVRRVID 60

Qy 61 IFDTDNGEVDVDFKEFTIEGVSQFSVKGDKQKLRFAFRIYDMDKDGYISNGELFQVLKMMV 120
 Db 61 VFDTDNGEVDVDFKEFTILGTSQFSVKGDEQKLRFAFSIYDMDKDGYISNGELFQVLKMMV 120

Qy 121 GNNLKDQLOQIVDKTIINADKDGGRISPEFCFCAVVGGLDIHKMMVVDV 170
 Db 121 GNNLTDWLOQLVDKTIILDKDGGKISPEFSAVVRDLRIHKKLVLIV 170

RESULT 9
 AAB64410
 ID AAB64410 standard; protein; 173 AA.
 XX
 AC AAB64410;
 XX
 DT 22-MAR-2001 (first entry)
 XX
 DE Amino acid sequence of human intracellular signalling molecule INTRA42.
 XX
 KW Human; intracellular signalling molecule; INTRA; immunosuppressive;
 KW cytostatic; neuroprotective; nootropic; antiarteriosclerotic; cancer;
 KW antiinflammatory; anti-HIV; neuroleptic; antibacterial; antifungal;
 KW antiviral; antiparasitic; antihelminthic; antiparkinsonian; AIDS;
 KW cell proliferative disorder; arteriosclerosis autoimmune; epilepsy;
 KW inflammatory disorder; Addison's disease; gastrointestinal disorder;
 KW neurological disorder; Parkinson's disease; Creutzfeldt-Jakob disease;
 KW mental disorder; schizophrenia; anxiety.
 XX
 OS Homo sapiens.
 XX
 FN WO200077040-A2.
 XX
 PD 21-DEC-2000.
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 PF 16-JUN-2000; 2000WO-US016636.
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 XX
 XX (INCY-) INCYTE GENOMICS INC.
 PA
 XX Yue H, Tang YT, Hillman JL, Lal P, Bandman O, Baughn MR;
 PI Azimzai Y, Yang J, Reddy R, Lu DAM;
 XX
 DR WPI; 2001-025334/03.
 DR N-PSDB; AAF32679.
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PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
(HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-581633/65.
XX N-PSDB; ABK43657.
XX
XX New isolated nucleic acid encoding a protein for diagnosing, preventing,
XX treating or ameliorating medical conditions and used as food additives or
XX preservatives.
XX
XX Claim 9; SEQ ID NO 845; 837pp; English.
XX
XX The invention describes an isolated nucleic acid molecule (I) encoding a
XX novel central nervous system protein. (I) and polypeptides (III) encoded

CC by (1), are used to treat a medical conditions and in diagnosis of a
CC pathological condition. Disorders which are diagnosed or treated include
CC autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative
CC disorders e.g. neoplasms of the breast or liver, cardiovascular disorders
CC e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia,
CC angiogenesis, nervous system disorders e.g. Alzheimer's disease and
CC amyotrophic lateral sclerosis, infections caused by bacteria, viruses
CC e.g. Acquired immunodeficiency virus (AIDS) and fungi, ocular disorders
CC e.g. corneal infection, gastrointestinal disorders e.g. dysphagia,
CC adenocarcinomas and irritable bowel syndrome, reproductive system
CC disorders e.g. testicular feminisation, endocrine disorders e.g. diabetes
CC and pituitary dwarfism, cancers and disorders at the cellular level e.g.
CC leukaemia, disorders involving neovascularisation e.g. malignancies,
CC respiratory disorders e.g. nonallergic rhinitis, renal disorders e.g.
CC acute kidney failure and blood related disorders e.g. myocardial
CC infarction. The polypeptides can also be used to aid wound healing and
CC epithelial cell proliferation, to prevent skin aging due to sunburn, to
CC maintain organs before transplantation, for supporting cell culture of
CC primary tissues, to regenerate tissues and in chemotaxis. The
CC polypeptides can also be used as a food additive or preservative to
CC increase or decrease storage capabilities, fat content, lipid, protein,

Query Match 84.3%; Score 738; DB 4; Length 187;
Best Local Similarity 84.7%; Pred. No. 7e-69;
Matches 144; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

Qy 1 MGNEASYPLEWCSHFDADAELKRLGKRPFKLLDLSNGSLSVVEFMSLPQLQNPVLQVRVID 60
Db 18 MGNEASYPACMSCHFNDKRLGRFRPKLLDLSKSLSVVEFMSLPRLHNPVLVRVID 77
Qy 61 IFDTDNGEVDKFEFIEGVQSFVKGDKEQKLFAPRIYDMDKDGYISNGELFVLKQMV 120
Db 78 VFDTDNGEVDKFEFIEGLTQSFVKGDDEQKLFAPRIYDMDKDGYISNGELFVLKQMV 137
Qy 121 GNNLKTQLQOIVDKTIINADKQDGRISFEFCVAVGGLDIHKKMVVDV 170
Db 138 GNNLTDWLQQLVDKTIILDKDGDGKISFEFSVAVRDLHKKVLIV 187

RESULT 12
ADI54642
ID ADI54642 standard; protein; 187 AA.

AC ADI54642;

DT 22-APR-2004 (first entry)

XX Novel human protein seq id 845.

XX neuroprotective; neurotropic; antiparkinsonian; anticonvulsant;
KW antidiabetic; antirheumatic; antiarthritic; dermatological;
KW antiinflammatory; immunosuppressive; antithyroid; antianemic; vasotropic;
KW anti-HIV; hepatotropic; virucide; antibacterial; fungicide;
KW antiparasitic; muscular; gynaecological; gastrointestinal; respiratory;
KW cardiovascular; antiarteriosclerotic; antiarrhythmic; cardiac;
KW nephrotropic; litholytic; cyostatic; gene therapy; neural disorder;
KW Alzheimer's disease; Parkinson's disease; Huntington's chorea;
KW amyotrophic lateral sclerosis; multiple sclerosis;
KW immune system disorder; diabetes; rheumatoid arthritis;
KW systemic lupus erythematosus; autoimmune thyroiditis; haemolytic anaemia;
KW inflammatory disorder; ischaemia-reperfusion injury;
KW inflammatory bowel disease; Crohn's disease; infectious disease;
KW HIV infection; hepatitis infection; bacterial infection;
KW fungal infection; parasitic infection; muscular disorder;
KW reproductive disorder; gastrointestinal disorder; pulmonary disorder;
KW cardiovascular disorder; atherosclerosis; arrhythmia; myocarditis;
KW renal disorder; acute glomerulonephritis; pyelonephritis;
KW renal lithiasis; proliferative disorder; cancerous diseases; human.

OS Homo sapiens.

XX US2004018969-A1.

PD 29-JAN-2004.
XX 17-JAN-2001; 2001US-00764875.
XX 31-JAN-2000; 2000US-0179065P.
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PR 05-DEC-2000; 2000US-0251988P.
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PR 11-DEC-2000; 2000US-0251990P.
PR 05-JAN-2001; 2001US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX (HUMA-) HUMAN GENOME SCI INC.
PA
XX
XX PI Rosen CA, Barash SC, Ruben SM;
XX
XX DR WPI; 2001-465570/50.
XX DR N-PSDB; AAL01209.
XX
PT Isolated nucleic acid molecule encoding a reproductive system antigen is
PT used in preventing, treating or ameliorating a medical condition.
XX Claim 11; SEQ ID NO 3897; 1297pp + Sequence Listing; English.
PS
XX The present invention provides the protein and coding sequences of a
CC number of human reproductive system related antigens. These can be used
CC in the prevention and treatment of reproductive system disorders,
CC including cancer. The present sequence is a protein of the invention
XX
XX SQ Sequence 189 AA;
Query Match 84.3%; Score 738; DB 4; Length 189;
Best Local Similarity 84.7%; Pred. No. 7.1e-69;
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Matches 144; Conservative 11; Mismatches 15; Indels 0; Gaps 0;	
Qy	1 MGNEASYPLEMCSDHDEIKRLGRFKKLDLNSGSLSVEEFMSLPELQONPLVORVID 60
Db	20 MGNEASYPAEMCSHFDNDEIKRLGRFKKLDLNSGSLSVEEFMSLPELRHNPVRRVID 79
Qy	61 IFDTGNGEVDPKFIEGVQSQSVKGDKEQKLRFAPRIYDMDKGYISNGELFQVLKMWV 120
Db	80 VFDTGDGEVDKFEILGTSQSVKGDKEQKLRFAPRIYDMDKGYISNGELFQVLKMWV 139
Qy	121 GNNLKDTOLQIVDKTIINADKDGGRISPEFCVAVGGLDIHKKMWVDV 170
Db	140 GNNLTDWQLQVLVDKTIILDKDGDGKISPEFSAVVRDLRIHKKLVLI 189
RESULT 14	
AAM43639	
ID	AAM43639 standard; protein; 189 AA.
XX	AC
XX	AAM43639;
XX	XX
DT	22-OCT-2001 (first entry)
XX	XX
DE	Human polypeptide SEQ ID NO 317.
XX	XX
KW	Human; antiarthritic; anti-rheumatic; antiproliferative; vasotropic; cerebrotective; neurotropic; neuroprotective; antibacterial; virucide; fungicide; ophthalmological; cytostatic; immunosuppressive; nootropic; neuroprotective; antiallergic; hepatotropic; antidiabetic; antinflammatory; antitumor; cancer; gene therapy; immune disorder; cardiovascular disorder; neurological disease; infection; human.
OS	Homo sapiens.
XX	XX
PN	WO200155308-A2.
XX	XX
PD	02-AUG-2001.
XX	XX
PF	17-JAN-2001; 2001WO-US001309.
XX	XX
PR	31-JAN-2000; 2000US-0179065P.
PR	04-FEB-2000; 2000US-0180628P.
PR	24-FEB-2000; 2000US-0184664P.
PR	02-MAR-2000; 2000US-0186350P.
PR	16-MAR-2000; 2000US-0189874P.
PR	17-MAR-2000; 2000US-0190076P.
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PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
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PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
XX
XX WPI; 2001-488781/53.
DR N-PSDB; AAI63870.
XX
XX New isolated nucleic acids and polypeptides, useful for diagnosing,
PT treating and/or preventing human diseases and disorders.
XX
XX Claim 11; SEQ ID NO 242; 664pp + Sequence Listing; English.

PS The invention relates to human polynucleotides (AAI63803-AAI64012) and
XX the encoded proteins (AAM434497-AAM43660) useful for preventing, treating
CC or ameliorating medical conditions e.g. by protein or gene therapy. The
CC genes were isolated from a range of human tissues disclosed in the
CC specification. The nucleic acids, proteins, antibodies and (ant)agonists
CC are useful in the diagnosis, treatment and prevention of: (a) cancer,
CC e.g. breast and ovarian cancer and other cancers of the adrenal gland,
CC bone, bone marrow, breast, gastrointestinal tract, liver, lung, or
CC urogenital; (b) immune disorders e.g. Addison's disease, allergies,
CC autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus,
CC Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative
CC colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d)
CC wound healing; (e) neurological diseases e.g. cerebral anoxia and
CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
CC and parasitic infections. Note: The sequence data for this patent did not
CC form part of the printed specification, but was obtained in electronic
CC format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX

SQ Sequence 189 AA;

Query Match 84.3%; Score 738; DB 4; Length 189;
Best Local Similarity 84.7%; Pred. No. 7.1e-69;
Matches 144; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

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Qy 61 IFDTGNGEVDKFEFIEGVSQFSVKGDKEQKLPFAPRIYDMDKDGYISNGELFQVLKQMV 120
Db 80 VFDTGNGEVDKFEFIEGVSQFSVKGDKEQKLPFAPRIYDMDKDGYISNGELFQVLKQMV 139
Qy 121 GNNLKDTQLQGIYVDKTIINADKDGGRISFEFCFVGGGLDIHKKQVVDV 170
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Search completed: February 26, 2005, 14:24:52
Job time : 61.073 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 26, 2005, 14:17:13 ; Search time 12.6569 Seconds
(without alignments)
1292.323 Million cell updates/sec

Title: US-09-435-257D-35
Perfect score: 875
Sequence: 1 MGNEASYPLEMCSHFDADA...EEFCVAVGGLDIHKRMVVDV 170

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	875	100.0	170	1	A33391
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3	870	99.4	170	1	JC1220
4	870	99.4	216	1	S42716
5	789	90.2	170	2	JC7242
6	771	88.1	170	2	JC5174
7	767	87.7	170	2	A44307
8	707	80.8	179	2	JC1221
9	704	80.5	176	2	JQ1232
10	704	80.5	369	2	T22708
11	620	70.9	165	2	P80261
12	530.5	60.6	174	2	T47245
13	496	56.7	175	2	JH0462
14	483	55.2	174	2	T41632
15	316.5	36.2	213	2	T31775
16	308.5	35.3	195	2	T28047
17	260	29.7	311	2	T21563
18	233.5	26.7	150	2	T07132
19	233.5	26.7	151	2	A71409
20	230	26.3	591	2	S54788
21	229.5	26.2	149	2	S35187
22	228.5	26.1	149	1	S53006
23	228.5	26.1	149	1	MCP2DC
24	228.5	26.1	149	1	S22503
25	228.5	26.1	149	1	S22971
26	228.5	26.1	149	1	S40301
27	228.5	26.1	149	1	S70768
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ALIGNMENTS

RESULT 1

A33391
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N:Alternate names: calcineurin beta subunit; calcineurin chain B; phosphoprotein phosphatase
C:Species: Homo sapiens (man)
C:Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 09-Jul-2004
C:Accession: A33391
R:Guerini, D.; Krinke, M.H.; Sikela, J.M.; Hahn, W.E.; Klee, C.B.
DNA 8, 675-682, 1989
A:Title: Isolation and sequence of a cDNA clone for human calcineurin B, the Ca(2+)-binding protein
A:Reference number: A33391; MUID:90126237; PMID:2558868
A:Accession: A33391
A:Molecule type: mRNA
A:Residues: 1-170 <GDE>
A:Cross-references: UNIPROT:P06705; GB:M30773; NID:g180704; PID:AAB08721.1; PID:g180705
C:Genetics:
A:Gene: GDB:PPP3R1; CALNB
A:Cross-references: GDB:l136804; OMIM:601302
A:Map position: 2p16-2p15
C:Complex: heterodimer with calcineurin catalytic chain
C:Superfamily: calmodulin; calmodulin repeat homology
C:Keywords: blocked amino end; calcium binding; duplication; EF hand; heterodimer; lipoprotein
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F:18-49/Domain: calmodulin repeat homology <EF1>
F:50-82/Domain: calmodulin repeat homology <EF2>
F:87-119/Domain: calmodulin repeat homology <EF3>
F:128-160/Domain: calmodulin repeat homology <EF4>
F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F:3/Modified site: aspartic acid (Asn) #status predicted
F:31,33,35,37,42/Binding site: calcium (Asp, Asp, Ser, Ser, Glu) #status predicted
F:63,65,67,69,74/Binding site: calcium (Asp, Asp, Asn, Glu, Glu) #status predicted
F:100,102,104,106,111/Binding site: calcium (Asp, Asp, Tyr, Glu) #status predicted
F:141,143,145,147,152/Binding site: calcium (Asp, Asp, Arg, Glu) #status predicted

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RESULT 2

S34127
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 N;Alternate names: calcineurin beta subunit; calcineurin chain B; phosphoprotein phosphatase
 C;Species: Bos primigenius taurus (cattle)
 C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
 C;Accession: I45831; J02097; S34127
 R;Nargang, C.E.; Bottorff, D.A.; Adachi, K.
 DNA Seq. 4, 313-318, 1994
 A;Title: Isolation and characterization of a cDNA clone coding for the calcium-binding subunit of calcineurin
 A;Reference number: I45831; MUID:95102111; PMID:7803816
 A;Accession: J02097
 A;Molecule type: mRNA
 A;Residues: 1-170 <NA2>
 A;Cross-references: UNIPROT:P06705; EMBL:X71666; NID:G312968; PIDN:CAA50659.1; PID:G312968
 R;Atken, A.; Klee, C.B.; Cohen, P.
 Eur. J. Biochem. 139, 663-671, 1984
 A;Title: The structure of the B subunit of calcineurin.
 A;Reference number: J02097; MUID:84132092; PMID:6321184
 A;Accession: J02097
 A;Molecule type: protein
 A;Residues: 2-11, M, 13-153, S, 155-169 <AIT>
 R;Griffith, J.P.; Kim, J.L.; Kim, E.E.; Sincchak, M.D.; Thomson, J.A.; Fitzgibbon, M.J.; submitted to the Brookhaven Protein Data Bank, August 1996
 A;Reference number: A66708; PDB:1TCO
 A;Contents: annotation; X-ray crystallography, 2.5 angstroms, residues 2-170
 R;Griffith, J.P.; Kim, J.L.; Kim, E.E.; Sincchak, M.D.; Thomson, J.A.; Fitzgibbon, M.J.; Cell 82, 507-522, 1995
 A;Title: X-ray structure of calcineurin inhibited by the immunophilin-immunosuppressant FK506
 A;Reference number: A56967; MUID:95360994; PMID:7543369
 A;Contents: annotation; X-ray crystallography, 2.5 angstroms
 C;Complex: heterodimer with calcineurin catalytic chain (see PIR:A56968)
 C;Superfamily: calmodulin; calmodulin repeat homology
 F;2-170/Product: calcineurin regulatory chain #status experimental <MAT>
 F;2-170/Domain: calmodulin repeat homology <EF1>
 F;50-82/Domain: calmodulin repeat homology <EF2>
 F;87-119/Domain: calmodulin repeat homology <EF3>
 F;128-160/Domain: calmodulin repeat homology <EF4>
 F;2/Modified site: myristylated amino end (Gly) (in mature form) #status experimental
 F;141,143,145,147,152/Binding site: calcium (Asp, Asp, Arg, Asp, Tyr, Glu) #status experimental

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Qy	61	IFDTGNGEVD	FKFEF	IGSV	QFSV	KGDK	QKLP	APF	RIY	DM	KD	GYISNGELFQVLKQMV 120
Db	61	IFDTGNGEVD	FKFEF	IGSV	QFSV	KGDK	QKLP	APF	RIY	DM	KD	GYISNGELFQVLKQMV 120
Qy	121	GNNLKDTQL	QQI	VDKTI	INAD	KD	GDGR	ISFE	EF	CA	VG	GLDIHKKMVDV 170
Db	121	GNNLKDTQL	QQI	VDKTI	INAD	KD	GDGR	ISFE	EF	CA	VG	GLDIHKKMVDV 170

RESULT 3
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 Calcineurin regulatory chain, brain - mouse
 N;Alternate names: calcineurin beta-1 subunit; calcineurin chain B-1; phosphoprotein phosphatase
 C;Species: Mus musculus (house mouse)
 C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
 C;Accession: JCI220
 R;Ueki, K.; Muramatsu, T.; Kincaid, R.L.
 Biochem. Biophys. Res. Commun. 187, 537-543, 1992
 A;Title: Structure and expression of two isoforms of the murine calmodulin-dependent protein kinase II

A;Reference number: JCI220; MUID:92392379; PMID:1325794
 A;Accession: JCI220
 A;Molecule type: mRNA
 A;Residues: 1-170 <UEK>
 A;Cross-references: UNIPROT:Q63810; GB:S43864; NID:G255078; PIDN:AAB23171.1; PID:G255078
 A;Experimental source: brain
 C;Comment: With calcineurin catalytic chain plays an important role in neural and nonneural functions
 C;Genetics:
 A;Gene: PP2B-beta-1
 A;Complex: heterodimer with calcineurin catalytic chain
 C;Superfamily: calmodulin; calmodulin repeat homology
 C;Keywords: blocked amino end; calcium binding; duplication; EF hand; heterodimer; lipoprotein
 F;2-170/Product: calcineurin regulatory chain #status predicted <MAT>
 F;18-49/Domain: calmodulin repeat homology <EF1>
 F;50-82/Domain: calmodulin repeat homology <EF2>
 F;87-119/Domain: calmodulin repeat homology <EF3>
 F;128-160/Domain: calmodulin repeat homology <EF4>
 F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted

Query Match 99.4%; Score 870; DB 1; Length 170;
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Qy	61	IFDTGNGEVD	FKFEF	IGSV	QFSV	KGDK	QKLP	APF	RIY	DM	KD	GYISNGELFQVLKQMV 120
Db	61	IFDTGNGEVD	FKFEF	IGSV	QFSV	KGDK	QKLP	APF	RIY	DM	KD	GYISNGELFQVLKQMV 120
Qy	121	GNNLKDTQL	QQI	VDKTI	INAD	KD	GDGR	ISFE	EF	CA	VG	GLDIHKKMVDV 170
Db	121	GNNLKDTQL	QQI	VDKTI	INAD	KD	GDGR	ISFE	EF	CA	VG	GLDIHKKMVDV 170

RESULT 4
 S42716
 Calcineurin regulatory chain, long splice form - rat
 N;Alternate names: calcineurin beta subunit; calcineurin chain B; phosphoprotein phosphatase
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
 C;Accession: S42716; S42717
 R;Chang, C.D.; Mukai, H.; Kuno, T.; Tanaka, C.
 Biochim. Biophys. Acta 1217, 174-180, 1994
 A;Title: cDNA cloning of an alternatively spliced isoform of the regulatory subunit of calcineurin
 A;Reference number: S42716; MUID:94153993; PMID:8110831
 A;Accession: S42716
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-216 <CHAL>
 A;Cross-references: UNIPROT:P06705; EMBL:D14425; NID:G286205; PIDN:BAA03318.1; PID:G286205
 A;Accession: S42717
 A;Molecule type: mRNA
 A;Residues: M, 48-216 <CH2>
 A;Cross-references: EMBL:D14568; NID:G286255; PIDN:BAA03422.1; PID:G286256
 C;Complex: heterodimer with calcineurin catalytic chain
 C;Superfamily: calmodulin; calmodulin repeat homology
 C;Keywords: alternative splicing; blocked amino end; calcium binding; duplication; EF hand; heterodimer; lipoprotein
 F;2-216/Product: calcineurin regulatory chain, long splice form #status predicted <MAT>
 F;48-216/Product: calcineurin regulatory chain, short splice form #status predicted <MAT>
 F;64-95/Domain: calmodulin repeat homology <EF1>
 F;96-128/Domain: calmodulin repeat homology <EF2>
 F;M, 48-216/Product: calcineurin regulatory chain, short splice form precursor #status predicted <MAT>
 F;133-165/Domain: calmodulin repeat homology <EF3>
 F;174-206/Domain: calmodulin repeat homology <EF4>
 F;48/Modified site: myristylated amino end (Gly) (in mature form) #status experimental
 F;49/Modified site: aspartic acid (Asn) #status predicted

Query Match 99.4%; Score 870; DB 1; Length 216;
 Best Local Similarity 100.0%; Pred. No. 9e-56;


```

A;Accession: PS0261
A:Molecule type: mRNA
A:Residues: 1-165 <SUG>
A:Cross-references: GB:S63991; NID:g238643; PIDN:AAB20281.1; PID:g238644
C:Superfamily: calmodulin; calmodulin repeat homology
C:Keywords: blocked amino end; calcium binding; duplication; EF hand
F:7-38/Domain: calmodulin repeat homology <EF1>
F:39-71/Domain: calmodulin repeat homology <EF2>
F:76-108/Domain: calmodulin repeat homology <EF3>
F:117-149/Domain: calmodulin repeat homology <EF4>

Query Match          70.9%; Score 620; DB 2; Length 165;
Best Local Similarity 82.4%; Pred. No. 6.4e-38;
Matches 122; Conservative 12; Mismatches 14; Indels 0; Gaps 0

Qy   23 LGRKFKLLDLNSGSLSEVEFMSPPELQQNPVQRVIDIFDTDNGGEVDKFKEFIGVSOF 82Z
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db   12 LGRSFKKMDLDSGSLSDVFMSLPPELQQNPVGRVIDIFDTDNGGEVDREFRIVGTSGF 7I

Qy   83 SVKGDEKEQLRFAPRIYDMDKGYISNGELFOVLKOMVGNNLKOTLOQIVDKTTINADK 14Z
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db   72 SVRGDEEQLRFAPRIYDMNDGFISNGELFOVLKOMVGNNLKWQLQOLVKLSILVLDK 13I

Qy   143 DGDGRISFEERCAVGGGLDIHKMWVDV 170
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db   132 DGDGRISFEERPDVVRTMEIHKKLVVF 159
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 12
T47245
calcinurin regulatory chain [imported] - Neurospora crassa
C:Species: Neurospora crassa
C>Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C:Accession: T47245
R:Dieminger, M.; Tropechug, M.
submitted to the EMBL Data Library, April 1997
A:Reference number: Z24421
A:Accession: T47245
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-174 <DIE>
A:Cross-references: UNIPROT:P87072; EMBL:Y12814; PIDN:CAA73345.1
A:Experimental source: strain 74 A
C:Genetics:
A:Gene: Can B
C:Superfamily: calmodulin; calmodulin repeat homology
C:Keywords: EF hand

Query Match          60.6%; Score 530.5; DB 2; Length 174;
Best Local Similarity 63.0%; Pred. No. 1.9e-31;
Matches 105; Conservative 28; Mismatches 36; Indels 3; Gaps 2

Qy   1 MGN-EASVP--LEMCSHFDADIKELGRFFKLKLDNSGSLSEVEFMSPPELQQNPVQR 57Z
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db   1 MGNTSSVPDNIVOGSNDFRBEVDLRKRFPWKLKDNSGTIEREEFLSLPQISTTNPLATR 60

Qy   58 VIDIFDTDNGGEVDKFKEFIGVSQFSVKGDKEQKLRFAPRIYDMDKDGYSINGELFOVLK 117
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db   61 MIALFDENGGDVDVFQEPVSGLSAFSRKGNKEQKLRFAPKVYDIDRDGYISNGELFIVLK 120

Qy   118 MMVGNNLKOTLOQIVDKTTINADKGDGRISFEERCAVGGGLDIHKMWVDV 169
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db   121 MMVGSNNLKDOOLRVYDKTIWEADLDKGGKSIFEERTKMVENTDYMSMTLD 17Z

```

RESULT 13
JH0462
phosphoprotein phosphatase regulatory chain - yeast (*Saccharomyces cerevisiae*)
N:Alternate names: calcineurin chain B homolog; protein phosphatase 2B chain B; protein C; Species: *Saccharomyces cerevisiae*
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C:Accession: JH0462; A45021; S33962; S38022; S34680; S52282
R:Kuno, T.; Tanaka, H.; Mukai, H.; Chang, C.D.; Hiraga, K.; Miyakawa, T.; Tanaka, C.

Biochem. Biophys. Res. Commun. 180, 1159-1163, 1991

A:Title: cDNA cloning of a calcineurin B homolog in Saccharomyces cerevisiae.

A:Reference number: JH0462; MUID:92062059; PMID:1659397

A:Accession: JH0462

A:Molecule type: mRNA

A:Residues: 1-175 <KUN>

A:Cross-references: UNIPROT:P25296; EMBL:D10293; NID:g218409; PIDN:BAA01136.1; PID:g2184

R:Cyert, M.S.; Thorner, J.

Mol. Cell. Biol. 12, 3460-3469, 1992

A:Title: Regulatory subunit (CNB1 gene product) of yeast Ca²⁺/calmodulin-dependent phosph

A:Reference number: A45021; MUID:92334345; PMID:1321337

A:Accession: A45021

A:Molecule type: DNA

A:Residues: 1-175 <CYB>

A:Cross-references: EMBL:M87508; NID:g171250; PIDN:AAA34505.1; PID:g171251

A:Note: sequence extracted from NCBI backbone (NCBIN:108731, NCBIP:108732)

R:Cheret, G.; Mattheakis, L.C.; Sor, F.

Yeast 9, 661-667, 1993

A:Title: DNA sequence analysis of the YCN2 region of chromosome XI in Saccharomyces cere

A:Reference number: S33960; MUID:93348778; PMID:8394042

A:Accession: S33962

A:Molecule type: DNA

A:Residues: 1-175 <CHE>

A:Cross-references: GB:X59765; NID:g296985; PIDN:CAA49421.1; PID:g296988

A:Experimental source: strain S288C

R:Wiemann, S.; Voss, H.; Schwager, C.; Rupp, T.; Grothues, D.; Senses, C.; Stegemann, J.

submitted to the Protein Sequence Database, March 1994

A:Reference number: S37825

A:Accession: S38022

A:Molecule type: DNA

A:Residues: 1-175 <WIE>

A:Cross-references: EMBL:Z28190; NID:g486336; PIDN:CAA82034.1; PID:g486337; MIPS:YKL190W

A:Experimental source: strain S288C

R:Maia e Silva, A.; Bossler, P.; Villela, C.; Fernandes, L.; Soares, H.; Guerreiro, P.; R

submitted to the Protein Sequence Database, March 1994

A:Reference number: S38024

A:Accession: S38027

A:Molecule type: DNA

A:Residues: 1-175 <MAI>

A:Cross-references: EMBL:Z28190; NID:g486336; PIDN:CAA82034.1; PID:g486337; MIPS:YKL190W

A:Experimental source: strain S288C

R:Wiemann, S.; Voss, H.; Schwager, C.; Rupp, T.; Stegemann, J.; Zimmermann, J.; Grothues

submitted to the EMBL Data Library, July 1993

A:Description: Sequencing and analysis of 51.5 kilobases on the left arm of chromosome X

A:Reference number: S34679

A:Accession: S34680

A:Molecule type: DNA

A:Residues: 31-175 <WIE>

A:Cross-references: EMBL:X74151; NID:g450365; PIDN:CAA52248.1; PID:g395235

A:Experimental source: strain S288C

R:Pardo, J.M.

submitted to the EMBL Data Library, September 1993

A:Description: The protein phosphatase calcineurin is essential for NaCl tolerance in Sa

A:Reference number: S52281

A:Accession: S52282

A:Molecule type: DNA

A:Residues: 1-175 <PAR>

A:Cross-references: EMBL:Z26521; NID:g473144; PIDN:CAA81290.1; PID:g473146

C:Genetics:

A:Gene: SGD:CNB1; YCN2

A:Cross-references: SGD:S0001673; MIPS:YKL190W

A:Map position: 11L

A:Introns: 18/1

C:Superfamily: calmodulin; calmodulin repeat homology

C:Keywords: blocked amino end; calcium binding; duplication; EF hand; heterodimer; lipop

F:2-175/Product: phosphoprotein phosphatase regulatory chain #status predicted <MAT>

F:21-52/Domain: calmodulin repeat homology <EF1>

F:53-85/Domain: calmodulin repeat homology <EF2>

F:90-122/Domain: calmodulin repeat homology <EF3>

F:121-163/Domain: calmodulin repeat homology <EF4>

F:12/Modified site: myristylated amino end (Gly) (in mature form) #status experimental

Query Match 56.7% Score 496; DB 2; Length 175;

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 26, 2005, 14:05:22 ; Search time 58.073 Seconds
(without alignments)
1499.035 Million cell updates/sec

Title: US-09-435-257D-35
Perfect score: 875
Sequence: 1 MGNRASYPLEMCSHPDADEI.....BEFCAVGGGLDIHKQMVVDV 170

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	875	100.0	170	Q66H20	Q66h20 brachydanio
2	875	100.0	170	Q6DJJ3	Q6dj33 xenopus lae
3	875	100.0	170	Q6VN50	Q6vn50 xenopus tro
4	875	100.0	170	Q6VN51	Q6vn51 gallus gall
5	870	99.4	169	1 CALB_BOVIN	P63099 bos taurus
6	870	99.4	169	1 CALB_HUMAN	P63098 homo sapien
7	870	99.4	169	1 CALB_RAT	P63100 rattus norv
8	865	98.9	169	1 CALB_MOUSE	Q70063 mus musculu
9	865	98.9	170	2 Q7T063	Q7t063 xenopus lae
10	796	91.0	170	2 Q9NKW7	Q9nk7 patinopecte
11	795	90.9	765	2 Q86Y00	Q86yq0 homo sapien
12	771	88.1	170	1 CALC_DROME	Q24214 drosophila
13	769	87.9	169	2 Q7PQ91	Q7pq91 anopheles g
14	767	87.7	170	1 CALB_DROME	P48451 drosophila
15	767	87.7	170	2 Q95P81	Q95p81 bombyx mori
16	739.5	84.5	169	2 Q86H16	Q86h16 schistosoma
17	737.5	84.3	169	2 Q9NFN1	Q9nfn1 schistosoma
18	733	83.8	169	1 CALC_HUMAN	Q96123 homo sapien
19	709	81.0	171	2 Q20804	Q20804 caenorhabdi
20	707	80.8	170	2 Q7YRC9	Q7yrc9 macaca mula
21	702	80.2	178	1 CALC_MOUSE	Q63811 mus musculu
22	699	79.9	175	2 CALC_RAT	P28470 rattus norv
23	580	66.3	115	2 Q99LQ9	Q99lq9 mus musculu
24	545.5	62.3	174	1 CALB_NEUCR	P87072 neurospora
25	544	62.2	173	1 CALB_YARLI	Q6cge6 yarrowia li
26	528	60.3	175	1 CALB_CRYNE	Q9hdel cryptococu
27	517	59.1	177	1 CALB_NAEGR	P42322 naegleria g
28	501.5	57.3	175	1 CALB_ASHGO	Q757b7 ashbya gos
29	496	56.7	174	1 CALB_YEAST	P25296 saccharomyc
30	483	55.2	174	1 CALB_SCHPO	Q9uu93 schistosacch
31	483	55.2	175	1 CALB_CANGA	Q6flu4 candida gla

32	475	54.3	175	1	CALB_KLULA
33	470.5	53.8	174	1	CALB_DEBHA
34	452.5	51.7	177	2	Q8MOT6
35	446	51.0	180	2	Q8GP83
36	445	50.9	169	2	Q867N3
37	436.5	49.9	177	2	Q86RA7
38	436	49.8	179	2	Q8IKV9
39	415.5	47.5	166	2	Q7RP38
40	372	42.5	175	2	Q9UOX7
41	340.5	38.9	194	1	CHP1_MOUSE
42	340.5	38.9	194	1	CHP1_RAT
43	338.5	38.7	193	2	Q6DK70
44	338.5	38.7	193	2	Q6DKL7
45	337.5	38.6	194	1	CHP1_HUMAN

ALIGNMENTS

RESULT 1
Q66H20 PRELIMINARY; PRT; 170 AA.
AC Q66H20;
DT 25-OCT-2004 (TRENBLrel. 28, Created)
DT 25-OCT-2004 (TRENBLrel. 28, Last sequence update)
DE ZGC:92169.
GN Name=zgc:92169;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=whole;
RX PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield V.S.,
RA Krzyzanski M.I., Skalska U., Smalls D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Mair M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=whole;
RX Director MGC Project;
RA Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC081617; AAH81617.1; -
DR InterPro; IPR001751; CaBP_S100.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR010983; EF-hand-like.
DR InterPro; IPR008080; Parvalbumin.
DR InterPro; IPR001125; Recoverin.
DR Pfam; PF00036; ehand; 4.
DR PRINTS; PR01697; PARVALBUMIN.
DR PRINTS; PR00450; RECOVERIN.
DR PRODom; PD003407; CaBP_S100; 1.
DR PRODom; PD000012; EF-hand; 2.

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DR SMART: SM00054; EFh; 4.
DR PROSITE: PS00018; EF HAND; 4.
SQ SEQUENCE 170 AA; 19300 MW; C904715DC0386056 CRC64;

Query Match 100.0%; Score 875; DB 2; Length 170;
Best Local Similarity 100.0%; Pred. No. 3.9e-52;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGNEASVPLEMCSHFDADKRLGKRFKPKLDLNSGSLSVVEEPMSPLELQONPLVQRVID 60
Db 1 MGNEASVPLEMCSHFDADKRLGKRFKPKLDLNSGSLSVVEEPMSPLELQONPLVQRVID 60
Qy 61 IFPTDGNGEVDKFEFIEGVSVKQKQKLFKFAFRIVDMDKGYISNGELFQVLKQMV 120
Db 61 IFPTDGNGEVDKFEFIEGVSVKQKQKLFKFAFRIVDMDKGYISNGELFQVLKQMV 120
Qy 121 GNNLKDTQLQOIYVDKTIINADKDGGRISFEFCVAVGGLDIHKKMVVDV 170
Db 121 GNNLKDTQLQOIYVDKTIINADKDGGRISFEFCVAVGGLDIHKKMVVDV 170

RESULT 2
Q6DJJ3 PRELIMINARY; PRT; 170 AA.
ID Q6DJJ3
AC Q6VNS0
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE MGC82148 protein.
GN Names=MGC82148;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative."
RL Dev. Dyn. 225:384-391(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Klein S., Gerhard D.S.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
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DR EMBL: BC075185; AAH75185.1; -.
DR GO: GO:0005509; F:calcium ion binding; IEA.
DR InterPro: IPR001751; CaBP_S100.
DR InterPro: IPR002048; EF-hand.
DR InterPro: IPR010983; EF-Hand like.
DR InterPro: IPR008080; Parvalbumin.
DR InterPro: IPR001125; Recoverin.
DR Pfam: PF00036; ehand; 4.
DR PRINTS: PR01697; PARVALBUMIN.
DR PRINTS: PR00450; RECOVERIN.
DR ProDom: PD003407; CaBP_S100; 1.
DR ProDom: PD000012; EF-hand; 2.
DR SMART: SM00054; EFh; 4.
DR PROSITE: PS00018; EF HAND; 4.
DR Calcium; Calcium-binding.
SQ SEQUENCE 170 AA; 19300 MW; C904715DC0386056 CRC64;

Query Match 100.0%; Score 875; DB 2; Length 170;
Best Local Similarity 100.0%; Pred. No. 3.9e-52;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGNEASVPLEMCSHFDADKRLGKRFKPKLDLNSGSLSVVEEPMSPLELQONPLVQRVID 60
Db 1 MGNEASVPLEMCSHFDADKRLGKRFKPKLDLNSGSLSVVEEPMSPLELQONPLVQRVID 60
Qy 61 IFPTDGNGEVDKFEFIEGVSVKQKQKLFKFAFRIVDMDKGYISNGELFQVLKQMV 120
Db 61 IFPTDGNGEVDKFEFIEGVSVKQKQKLFKFAFRIVDMDKGYISNGELFQVLKQMV 120
Qy 121 GNNLKDTQLQOIYVDKTIINADKDGGRISFEFCVAVGGLDIHKKMVVDV 170
Db 121 GNNLKDTQLQOIYVDKTIINADKDGGRISFEFCVAVGGLDIHKKMVVDV 170

RESULT 3
Q6VNS0 PRELIMINARY; PRT; 170 AA.
ID Q6VNS0
AC Q6VNS0
DT 03-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Protein phosphatase 3 regulatory subunit B alpha isoform type 1
DE (Hypothetical protein MGC75600).
GN Names=MGC75600;
OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8364;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhou G., Li W., Yu L., Zhao S.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Touchman J.W., Green E.D., Dickinson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
```


RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RL and mouse cDNA sequences.";
 RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RA Klein S., Gerhard D.S.;
 RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY336972; AAQ16148.1; -;
 DR EMBL; BC064854; AAH64854.1; -;
 DR HSSP; P02618; 1BR.
 DR GO; GO:0005509; F:calcium ion binding; IEA.
 DR InterPro; IPR001751; CAbP_S100.
 DR InterPro; IPR002048; EF-hand.
 DR InterPro; IPR010983; EF Hand like.
 DR InterPro; IPR008080; Parvalbumin.
 DR InterPro; IPR001125; Recoverin.
 DR Pfam; PF00036; ehand; 4.
 DR PRINTS; PR01697; PARVALBUMIN.
 DR PRODOM; PD00450; RECOVERIN.
 DR PRODOM; PD003407; CAbP_S100; 1.
 DR SMART; SM00054; EFh; 4.
 DR PROSITE; PS00018; EF HAND; 4.
 DR SMART; SM00054; EFh; 4.
 DR PROSITE; PS00018; EF HAND; 4.
 KW Calcium; Calcium-binding; Hypothetical protein.
 SQ SEQUENCE 170 AA; 19300 MW; C904715DC0386056 CRC64;

 Query Match 100.0%; Score 875; DB 2; Length 170;
 Best Local Similarity 100.0%; Pred. No. 3.9e-52;
 Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 1 MGNEASYLEPMSCHFDADETKRLGKRFKKLDLNSGSLSVVEFMSLPQLQNPVLRVID 60
 DB 1 MGNEASYLEPMSCHFDADETKRLGKRFKKLDLNSGSLSVVEFMSLPQLQNPVLRVID 60

 QY 61 IFDTGNGEVDKFEFIEGVSQFSVKGDKQKLRFAFRIYDMKDGYSINGSLFQVLKMW 120
 DB 61 IFDTGNGEVDKFEFIEGVSQFSVKGDKQKLRFAFRIYDMKDGYSINGSLFQVLKMW 120

 QY 121 GNNLKDTQLQIQIVDKTIINADKDGGRISPEFCVAVGGLDIHKKMWVDV 170
 DB 121 GNNLKDTQLQIQIVDKTIINADKDGGRISPEFCVAVGGLDIHKKMWVDV 170

 RESULT 4
 Q6VN51 PRELIMINARY; PRT; 170 AA.
 AC Q6VN51
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DE Protein phosphatase 3 regulatory subunit B alpha isoform type 1.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Bursa;
 RA Zhou G., Li W., Yu L., Zhao S.;
 RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY336970; AAQ16146.1; -;
 DR HSSP; P02618; 1BR.
 DR GO; GO:0005509; F:calcium ion binding; IEA.
 DR InterPro; IPR001751; CAbP_S100.
 DR InterPro; IPR002048; EF-hand.
 DR InterPro; IPR010983; EF Hand like.
 DR InterPro; IPR008080; Parvalbumin.
 DR InterPro; IPR001125; Recoverin.
 DR Pfam; PF00036; ehand; 4.
 DR PRINTS; PR01697; PARVALBUMIN.

 Query Match 100.0%; Score 875; DB 2; Length 170;
 Best Local Similarity 100.0%; Pred. No. 3.9e-52;
 Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 1 MGNEASYLEPMSCHFDADETKRLGKRFKKLDLNSGSLSVVEFMSLPQLQNPVLRVID 60
 DB 1 MGNEASYLEPMSCHFDADETKRLGKRFKKLDLNSGSLSVVEFMSLPQLQNPVLRVID 60

 QY 61 IFDTGNGEVDKFEFIEGVSQFSVKGDKQKLRFAFRIYDMKDGYSINGSLFQVLKMW 120
 DB 61 IFDTGNGEVDKFEFIEGVSQFSVKGDKQKLRFAFRIYDMKDGYSINGSLFQVLKMW 120

 QY 121 GNNLKDTQLQIQIVDKTIINADKDGGRISPEFCVAVGGLDIHKKMWVDV 170
 DB 121 GNNLKDTQLQIQIVDKTIINADKDGGRISPEFCVAVGGLDIHKKMWVDV 170

 RESULT 5
 CALB_BOVIN STANDARD; PRT; 169 AA.
 AC CALB_BOVIN
 DT 01-JAN-1998 (Rel. 06, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Calcineurin B subunit isoform 1 (protein phosphatase 2B regulatory
 DE subunit 1) (Protein phosphatase 3 regulatory subunit B alpha isoform
 DE 1).
 GN Name=PPP3R1; Synonyms=CNA2, CNB;
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Nargang C.E., Bottorff D.A., Adachi K.;
 RA "Isolation and characterization of a cDNA clone coding for the
 RT calcium-binding subunit of calcineurin from bovine brain: an identical
 RT amino acid sequence to the human protein.";
 RL DNA Seq. 4:313-318(1994).
 RN [2]
 RP SEQUENCE OF 1-168.
 RC TISSUE=Brain;
 RX MEDLINE=84132092; PubMed=6321184;
 RA Aitken A., Klee C.B., Cohen P.;
 RT "The structure of the B subunit of calcineurin.";
 RL Eur. J. Biochem. 139:663-671(1984).
 RN [3]
 RP CALCIUM-BINDING DATA.
 RX MEDLINE=80101597; PubMed=293720;
 RA Klee C.B., Crouch T.H., Krinks M.H.;
 RT "Calcineurin: a calcium- and calmodulin-binding protein of the nervous
 RT system.";
 RL Proc. Natl. Acad. Sci. U.S.A. 76:6270-6273(1979).
 RN [4]
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) IN COMPLEX WITH FKBP1A.
 RX MEDLINE=95360994; PubMed=7543369; DOI=10.1016/0092-8674(95)90439-5;
 RA Griffith J.P., Kim J.L., Kim E.E., Sintchak M.D., Thomson J.A.,
 RA Fitzgibbon M.J., Fleming M.A., Caron P.R., Hsiao K., Navia M.A.;
 RT "X-ray structure of calcineurin inhibited by the immunophilin-
 RT immunosuppressant FKBP12-FK506 complex.";
 RL Cell 82:507-522(1995).
 CC -!- FUNCTION: Regulatory subunit of calcineurin, a calcium-dependent,

calmodulin stimulated protein phosphatase. Confers calcium sensitivity.

-1- SUBUNIT: Composed of a catalytic subunit (A) and a regulatory subunit (B).

-1- MISCELLANEOUS: This protein has four functional calcium-binding sites.

-1- SIMILARITY: Contains 4 EF-hand calcium-binding domains.

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EMBL; X71666; CAA50659.1; -.
 PDB; 1TC0; X-ray; B=1-169.
 GO; GO:0005955; C:calcineurin complex; NAS.
 GO; GO:0005509; F:calcium ion binding; NAS.
 GO; GO:0004723; F:calcium-dependent protein serine/threonine . . .; NAS.
 GO; GO:0005517; F:calmodulin inhibitor activity; NAS.
 InterPro; IPR010983; EF-hand.
 InterPro; IPR008080; Parvalbumin.
 InterPro; IPR001125; Recoverin.
 Pfam; PF00036; ehand; 4.
 PRINTS; PR01697; PARVALBUMIN.
 PRINTS; PR00450; RECOVERIN.
 PROSITE; PS00018; EF HAND; 4.
 3D-structure; Calcium-binding; Direct protein sequencing; Lipoprotein; Myristate; Repeat.

INIT MET 0 0
 LIPID 1 1 N-myristoyl glycine.
 CA_BIND 30 41 EF-hand 1.
 CA_BIND 62 73 EF-hand 2.
 CA_BIND 99 110 EF-hand 3.
 CA_BIND 140 151 EF-hand 4.
 CONFLICT 11 11 C -> M (in Ref. 2).
 CONFLICT 153 153 C -> S (in Ref. 2).
 HELIX 16 29
 TURN 31 32
 TURN 36 37
 STRAND 39 42
 HELIX 43 44
 TURN 46 49
 HELIX 50 50
 TURN 52 53
 TURN 54 61
 TURN 63 64
 STRAND 69 70
 TURN 71 78
 HELIX 79 81
 TURN 83 84
 TURN 87 98
 TURN 100 101
 STRAND 105 106
 TURN 108 119
 TURN 120 121
 TURN 125 139
 TURN 141 142
 STRAND 147 148
 HELIX 149 156
 TURN 157 159
 HELIX 161 164
 SEQUENCE 169 AA; 19169 MW; 749141BD0434C90C CRC64;

Query Match 99.4%; Score 870; DB 1; Length 169;
 Best local similarity 100.0%; Pred. No. 8.5e-52;
 Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 GNEASYPLEMCSHFDADEIKRLGKRFKLDLNSGSLSVSEFMSLPQLQNPLVQRVIDI 60
 QY 62 FDTGNGEVDFKEFIEGVQSFVKGEKQLFAFRIYMDKGYISNGELFQVLKMWVG 121
 Db 61 FDTGNGEVDFKEFIEGVQSFVKGEKQLFAFRIYMDKGYISNGELFQVLKMWVG 120
 QY 122 NNLDKDTQLQOIYVDKTIINADKDGGRISPEEFCAVVGGLDIHKMVDV 170
 Db 121 NNLDKDTQLQOIYVDKTIINADKDGGRISPEEFCAVVGGLDIHKMVDV 169

RESULT 6
 CALB_HUMAN STANDARD; PRT; 169 AA.
 AC P63098; P06705; P15117; Q08044;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Calcineurin B subunit isoform 1 (Protein phosphatase 2B regulatory subunit 1) (Protein phosphatase 3 regulatory subunit B alpha isoform 1).
 GN Name=PPP3R1; Synonyms=CNA2, CNB;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90126237; PubMed=2558868;
 RA Guerini D., Krinks M.H., Sikela J.M., Hahn W.E., Klee C.B.;
 RT "Isolation and sequence of a cDNA clone for human calcineurin B, the
 RT Ca2+-binding subunit of the Ca2+/calmodulin-stimulated protein
 RT phosphatase.";
 RL DNA 8:675-682(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Ebert L., Schick M., Neubert P., Schatten R., Henze S., Korn B.;
 RT "Cloning of human full open reading frames in Gateway(TM) system entry
 RT vector (pDONR201).";
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Blood;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426030999;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Heiton E., Kettelman M., Maman A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [4]
 RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
 RX MEDLINE=96097077; PubMed=8524402; DOI=10.1038/378641a0;
 RA Kissinger C.R., Parge H.E., Knighton D.R., Lewis C.T., Pelletier L.A.,
 RA Tempczyk A., Kalish V.J., Tucker K.D., Showalter R.E., Moonaw E.W.,
 RA Gastinel L.N., Habuka N., Chen X., Maldonado F., Barker J.E.,
 RA Bacquet R., Villafranca J.E.;
 RT "Crystal structures of human calcineurin and the human FKBP12-FK506-

calcineurin complex.";
 RL Nature 378:641-644 (1995).
 [5]
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) IN COMPLEX WITH PP1A.
 RX PubMed=12218175; DOI=10.1073/pnas.192206699;
 RA Huai Q., Kim H.Y., Liu Y., Zhao Y., Mondragon A., Liu J.O., Ke H.;
 RT "Crystal structure of calcineurin-cyclophilin-cyclosporin shows common
 but distinct recognition of immunophilin-drug complexes.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:12037-12042 (2002).
 [6]
 RP X-RAY CRYSTALLOGRAPHY (3.1 ANGSTROMS) IN COMPLEX WITH PP1A.
 RX PubMed=12357034; DOI=10.1073/pnas.212504399;
 RA Jin L., Harrison S.C.;
 RT "Crystal structure of human calcineurin complexed with cyclosporin A
 and human cyclophilin.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:13522-13526 (2002).
 CC -!- FUNCTION: Regulatory subunit of calcineurin, a calcium-dependent,
 calmodulin stimulated protein phosphatase. Confers calcium
 sensitivity.
 CC -!- SUBUNIT: Composed of a catalytic subunit (A) and a regulatory
 subunit (B).
 CC -!- MISCELLANEOUS: This protein has four functional calcium-binding
 sites.
 CC -!- SIMILARITY: Contains 4 EF-hand calcium-binding domains.
 CC
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 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; M30773; AAB08721.1; -;
 DR EMBL; BC027913; AAB27913.1; -;
 DR EMBL; CR456938; CAG33219.1; -;
 DR PIR; A33391; A33391.
 DR PDB; 1AUI; X-ray; B=1-169.
 DR PDB; 1M63; X-ray; B/F=1-169.
 DR PDB; 1MF8; X-ray; B=1-169.
 DR OGP; P63098; -
 DR Genew; HGNC:9317; PPP3R1.
 DR MIM; 601302; -;
 DR GO; GO:0005955; C:calcineurin complex; NAS.
 DR GO; GO:0005909; F:calcium ion binding; NAS.
 DR GO; GO:0004723; F:calcium-dependent protein serine/threonine . . .; NAS.
 DR GO; GO:0005517; F:calmodulin inhibitor activity; NAS.
 DR InterPro; IPR002048; EF-hand.
 DR InterPro; IPR010983; EF-hand-like.
 DR InterPro; IPR008080; Parvalbumin.
 DR InterPro; IPR001125; Recoverin.
 DR Pfam; PF00036; ehand; 4.
 DR PRINTS; PR01697; PARVALBUMIN.
 DR PRINTS; PR00450; RECOVERIN.
 DR PROSITE; PS00018; EF HAND; 4.
 KW 3D-structure; Calcium-binding; Lipoprotein; Myristate; Repeat.
 FT INIT MET 0 0
 FT LIPID 1 1
 FT CA_BIND 30 41
 FT CA_BIND 62 73
 FT CA_BIND 99 110
 FT CA_BIND 140 151
 FT HELIX 16 29
 FT TURN 31 32
 FT TURN 36 37
 FT STRAND 39 42
 FT HELIX 43 44
 FT TURN 46 49
 FT TURN 50 53
 FT TURN 52 55
 FT HELIX 54 61
 FT TURN 63 64
 FT STRAND 69 70

FT HELIX 71 78
 FT HELIX 79 81
 FT TURN 83 84
 FT HELIX 87 98
 FT TURN 100 101
 FT STRAND 105 106
 FT HELIX 108 119
 FT TURN 120 121
 FT HELIX 125 139
 FT TURN 141 142
 FT STRAND 147 148
 FT HELIX 149 156
 FT HELIX 157 159
 FT HELIX 161 164
 SQ SEQUENCE 169 AA; 19169 MW; 749141BD0434C90C CRC64;
 Query Match 99.4%; Score 870; DB 1; Length 169;
 Best Local Similarity 100.0%; Pred. No. 8.5e-52;
 Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 GNEASYPLEMCSHFDADDEIKELGKRFKKLDLDNSGSLSVSEFMSLPELQQNPLVQRVIDI 61
 DB 1 GNEASYPLEMCSHFDADDEIKELGKRFKKLDLDNSGSLSVSEFMSLPELQQNPLVQRVIDI 60
 QY 62 PDTGNGEVDPKFIEGVQSFSVKGDKQKLRPAFRIYDMKDGYSINGELFQVLKMWVG 121
 DB 61 PDTGNGEVDPKFIEGVQSFSVKGDKQKLRPAFRIYDMKDGYSINGELFQVLKMWVG 120
 QY 122 NNLKDTOLQIVDKTIINADKDGGRISFEFCFCAVGGLDTHKKMWVDV 170
 DB 121 NNLKDTOLQIVDKTIINADKDGGRISFEFCFCAVGGLDTHKKMWVDV 169
 RESULT 7
 CALB_RAT
 ID - CALB_RAT STANDARD; PRT; 169 AA.
 AC P63100; P06705; P15117; Q08044;
 DT 01-JAN-1988 (Rel. 05, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Calcineurin B subunit isoform 1 (Protein phosphatase 2B regulatory
 subunit 1) (Protein phosphatase 3 regulatory subunit B alpha isoform
 1).
 GN Name=Ppp3r1; Synonyms=Cna2, Cnb;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OK NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC STRAIN=Fischer;
 RA Perrino B.A., Huang X., Ng L.Y., Soderling T.R.;
 RT "Regulation of calcineurin phosphatase activity by the B subunit and
 carboxy-terminal inhibitory domains of the A subunit.";
 RL Submitted (OCT-1992) to the EMBL/GenBank/DBJ databases.
 [2]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND TISSUE SPECIFICITY.
 RC TISSUE=Brain, and Testis;
 RX MEDLINE=94153993; PubMed=8110831; DOI=10.1016/0167-4781(94)90031-0;
 RA Chang C.-D., Mukai H., Kuno T., Tanaka C.;
 RT "cDNA cloning of an alternatively spliced isoform of the regulatory
 subunit of Ca2+/calmodulin-dependent protein phosphatase (calcineurin
 B alpha 2)".
 RL Biochim. Biophys. Acta 1217:174-180 (1994).
 CC -!- FUNCTION: Regulatory subunit of calcineurin, a calcium-dependent,
 calmodulin stimulated protein phosphatase. Confers calcium
 sensitivity.
 CC -!- SUBUNIT: Composed of a catalytic subunit (A) and a regulatory
 subunit (B).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=P63100-1, P06705-1;
 CC

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CC CC      Sequence=Displayed;
CC CC      Name=2;
CC CC      IsoId=P63100-2, P06705-2;
CC CC      Sequence=VSP_000729;
CC CC      TISSUE SPECIFICITY: Isoform 2 is testis specific.
CC CC      -1- MISCELLANEOUS: This protein has four functional calcium-binding
CC CC      sites.
CC CC      -1- SIMILARITY: Contains 4 EF-hand calcium-binding domains.
CC CC      -----
CC CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC CC      or send an email to license@isb-sib.ch).
CC CC      -----
CC CC      EMBL; L03554; AAA04854.1; -.
CC CC      EMBL; D14568; BAA03422.1; -.
CC CC      EMBL; D14425; BAA03318.1; -.
CC CC      PIR; S42716; S42716.
CC CC      RGD; 692330; Ppp3r1.
CC CC      GO; GO:0005955; C:calcineurin complex; NAS.
CC CC      GO; GO:0005509; F:calcium ion binding; NAS.
CC CC      GO; GO:0004723; F:calcium-dependent protein serine/threonine . . .; NAS.
CC CC      GO; GO:0005517; F:calmodulin inhibitor activity; NAS.
CC CC      InterPro; IPR002048; EF-hand.
CC CC      InterPro; IPR010983; EF-hand.
CC CC      InterPro; IPR008080; Parvalbumin.
CC CC      InterPro; IPR001125; Recoverin.
CC CC      Pfam; PF00036; ehand; 4.
CC CC      PRINTS; PR01697; PARVALBUMIN.
CC CC      PRINTS; PR00450; RECOVERIN.
CC CC      PROSITE; PS00019; EF_HAND; 4.
CC CC      KW      Alternative splicing; Calcium-binding; Lipoprotein; Myristate; Repeat.
CC CC      INIT MET 0 0 By similarity.
CC CC      FT LIPID 1 1 N-myristoyl glycine (By similarity).
CC CC      FT CA_BIND 30 41 EF-hand 1.
CC CC      FT CA_BIND 62 73 EF-hand 2.
CC CC      FT CA_BIND 99 110 EF-hand 3.
CC CC      FT CA_BIND 140 151 EF-hand 4.
CC CC      FT VARSPLIC 1 1
CC CC      FT FTID=VSP_000729.
CC CC      SQ      SEQUENCE 169 AA; 19169 MW; 749141BD0434C90C CRC64;
CC CC      Query Match 99.4%; Score 870; DB 1; Length 169;
CC CC      Best Local Similarity 100.0%; Pred. No. 8.5e-52;
CC CC      Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC CC      QY      2 GNEASYPLEMCSHFDADEIKRLGKRFKFKLDLDNSGSLSVSEEFMSLPQLQNPVQRVIDI 61
CC CC      DB      1 GNEASYPLEMCSHFDADEIKRLGKRFKFKLDLDNSGSLSVSEEFMSLPQLQNPVQRVIDI 60
CC CC      QY      62 FDTDNGEVDFKFEIEGVQSFVKGDKEQKLRFAFRIDYMDKGYISNGELFQVLKQMVG 121
CC CC      DB      61 FDTDNGEVDFKFEIEGVQSFVKGDKEQKLRFAFRIDYMDKGYISNGELFQVLKQMVG 120
CC CC      QY      122 NNLKDTQLQOIYDKTIINADKDGGRISFEFCVAVGGGLDIHKMVDV 170
CC CC      DB      121 NNLKDTQLQOIYDKTIINADKDGGRISFEFCVAVGGGLDIHKMVDV 169
CC CC      RESULT 8
CC CC      CALB_MOUSE STANDARD; PRT; 169 AA.
CC CC      AC Q63810;
CC CC      DT 01-NOV-1997 (Rel. 35, Created)
CC CC      DT 01-NOV-1997 (Rel. 35, Last sequence update)
CC CC      DT 25-OCT-2004 (Rel. 45, Last annotation update)
CC CC      DE Calcineurin B subunit isoform 1 (Protein phosphatase 2B regulatory
CC CC      DE subunit 1) (Protein phosphatase 3 regulatory subunit B alpha isoform
CC CC      DE 1).

```

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GN OS      Name=Ppp3r1; Synonyms=Cnb;
OC OS      Mus musculus (Mouse).
OC OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC RN      NCBI_TaxID=10090;
RN RN      [1]
RP RP      SEQUENCE FROM N.A.
RC RC      TISSUE=Brain;
RX RX      MEDLINE=92392379; PubMed=1325794;
RA RA      Ueki K., Muramatsu T., Kincaid R.L.;
RT RT      "Structure and expression of two isoforms of the murine calmodulin-
RL RL      dependent protein phosphatase regulatory subunit (calcineurin B).";
RL RL      Biochem. Biophys. Res. Commun. 187:537-543(1992).
CC CC      -1- FUNCTION: Regulatory subunit of calcineurin, a calcium-dependent,
CC CC      calmodulin stimulated protein phosphatase. Confers calcium
CC CC      sensitivity.
CC CC      -1- SUBUNIT: Composed of a catalytic subunit (A) and a regulatory
CC CC      subunit (B).
CC CC      -1- TISSUE SPECIFICITY: Brain specific.
CC CC      -1- MISCELLANEOUS: This protein has four functional calcium-binding
CC CC      sites.
CC CC      -1- SIMILARITY: Contains 4 EF-hand calcium-binding domains.
CC CC      -----
CC CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC CC      the European Bioinformatics Institute. There are no restrictions on its
CC CC      use by non-profit institutions as long as its content is in no way
CC CC      modified and this statement is not removed. Usage by and for commercial
CC CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC CC      or send an email to license@isb-sib.ch).
CC CC      -----
CC CC      EMBL; S43864; AAB23171.1; -.
CC CC      PIR; JC1220; JC1220.
CC CC      HSP; P06705; IAU1.
CC CC      MGD; MGI:107172; Ppp3r1.
CC CC      InterPro; IPR002048; EF-hand.
CC CC      InterPro; IPR010983; EF-hand like.
CC CC      InterPro; IPR008080; Parvalbumin.
CC CC      InterPro; IPR001125; Recoverin.
CC CC      Pfam; PF00036; ehand; 4.
CC CC      PRINTS; PR01697; PARVALBUMIN.
CC CC      PRINTS; PR00450; RECOVERIN.
CC CC      ProDom; PD003407; CabP S100; 1.
CC CC      ProDom; PD000012; EF-hand; 2.
CC CC      PROSITE; PS00018; EF_HAND; 4.
CC CC      KW      Calcium-binding; Lipoprotein; Myristate; Repeat.
CC CC      INIT MET 0 0 By similarity.
CC CC      FT LIPID 1 1 N-myristoyl glycine (By similarity).
CC CC      FT CA_BIND 30 41 EF-hand 1.
CC CC      FT CA_BIND 62 73 EF-hand 2.
CC CC      FT CA_BIND 99 110 EF-hand 3.
CC CC      FT CA_BIND 140 151 EF-hand 4.
CC CC      SQ      SEQUENCE 169 AA; 19142 MW; D1490BA5BD2F432F CRC64;
CC CC      Query Match 98.9%; Score 865; DB 1; Length 169;
CC CC      Best Local Similarity 99.4%; Pred. No. 1.9e-51;
CC CC      Matches 168; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
CC CC      QY      2 GNEASYPLEMCSHFDADEIKRLGKRFKFKLDLDNSGSLSVSEEFMSLPQLQNPVQRVIDI 61
CC CC      DB      1 GSEASYPLEMCSHFDADEIKRLGKRFKFKLDLDNSGSLSVSEEFMSLPQLQNPVQRVIDI 60
CC CC      QY      62 FDTDNGEVDFKFEIEGVQSFVKGDKEQKLRFAFRIDYMDKGYISNGELFQVLKQMVG 121
CC CC      DB      61 FDTDNGEVDFKFEIEGVQSFVKGDKEQKLRFAFRIDYMDKGYISNGELFQVLKQMVG 120
CC CC      QY      122 NNLKDTQLQOIYDKTIINADKDGGRISFEFCVAVGGGLDIHKMVDV 170
CC CC      DB      121 NNLKDTQLQOIYDKTIINADKDGGRISFEFCVAVGGGLDIHKMVDV 169
CC CC      RESULT 9
CC CC      Q7T063

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ID Q7T063 PRELIMINARY; PRT; 170 AA.
 AC Q7T063;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Protein phosphatase 3 regulatory subunit B alpha isoform type 1
 DE (Hypothetical protein).
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zhou G., Li W., Yu L., Zhao S.;
 RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 EX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
 RA Richardson P.;
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
 RT initiative.";
 RL Dev. Dyn. 225:384-391 (2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 EX PubMed=12471932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettner M., Madan A.C., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RA Klein S., Gerhard D.S.;
 RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY336971; AAQ16147.1; -;
 DR EMBL; BC082858; AA082858.1; -;
 DR HSSP; P07463; INOY.
 DR GO; GO:0005509; F:calcium ion binding; IEA.
 DR InterPro; IPR001751; CAP_S100.
 DR InterPro; IPR002048; EF-hand.
 DR InterPro; IPR010983; EF_Hand_like.
 DR Pfam; PF00036; ehand; 4.
 DR ProDom; PD03407; CAP_S100; 1.
 DR ProDom; PD000012; EF-hand; 2.
 DR SMART; SM00054; EFh; 4.
 DR PROSITE; PS00018; EF_HAND; 4.
 KW Calcium; Calcium-binding; Hypothetical protein.
 SQ SEQUENCE 170 AA; 19328 MW; EFDD715DD8A9E956 CRC64;

Query Match 98.9%; Score 865; DB 2; Length 170;
 Best Local Similarity 98.2%; Pred. No. 1.9e-51;
 Matches 167; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGNEASYPLEMCSHFDADEIKRLGKRFKGLDLDNSGSLSVVEFMSPLELQNPVLQVRVID 60
 Db |||||
 QY 1 MGNEASYPLEMCSHFDADEIKRLGKRFKGLDLDNSGSLSVVEFMSPLELQNPVLQVRVID 60
 Db |||||
 QY 61 IFDTDNGEVDPFKEFIEGVQSFSVKGDKLRFAPRIYDMDKGYISNGELFQVLKQMV 120
 Db |||||
 QY 61 IFDTDNGEVDPFKEFIEGVQSFSVKGDKLRFAPRIYDMDKGYISNGELFQVLKQMV 120
 Db |||||
 QY 121 GNNLKDTQLQOI VDKTIINADKDGRI SPFEFCVAVGGLDIHKQMVVDV 170
 Db |||||
 QY 121 GNNLKDTQLQOI VDKTIINADKDGRI SPFEFCVAVGGLDIHKQMVVDV 170
 Db |||||

RESULT 10
Q9NKW7

ID Q9NKW7 PRELIMINARY; PRT; 170 AA.
 AC Q9NKW7;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Calcineurin B.
 OS Patinopecten yessoensis (Ezo giant scallop) (Yesso scallop).
 OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Pectinoida;
 OC Pectinoidea; Pectinidae; Mizuhopecten.
 OX NCBI_TaxID=6573;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RA Uryu M., Nakatomi A., Watanabe M., Hatause R., Yazawa M.;
 RT "Molecular Cloning of cDNA Encoding Two Subunits of Calcineurin from
 RT Scallop Testis: Demonstration of Stage-Specific Expression during
 RT Maturation of the Testis.";
 RL J. Biochem. 0:0-0 (2000).
 DR EMBL; AB041524; BAA94543.1; -;
 DR PIR; JC7242; JC7242.
 DR HSSP; P41208; IM39.
 DR GO; GO:0005509; F:calcium ion binding; IEA.
 DR InterPro; IPR002048; EF-hand.
 DR InterPro; IPR010983; EF_Hand_like.
 DR InterPro; IPR008080; Parvalbumin.
 DR InterPro; IPR001125; Recoverin.
 DR Pfam; PF00036; ehand; 4.
 DR PRINTS; PR01697; PARVALBUMIN.
 DR PRINTS; PR00450; RECOVERIN.
 DR SMART; SM00054; EFh; 4.
 DR PROSITE; PS00018; EF_HAND; 4.
 KW Calcium; Calcium-binding.
 SQ SEQUENCE 170 AA; 19238 MW; 9450322698470F44 CRC64;

Query Match 91.0%; Score 796; DB 2; Length 170;

Best Local Similarity 89.4%; Pred. No. 9.2e-47;
 Matches 152; Conservative 11; Mismatches 7; Indels 0; Gaps 0;

QY 1 MGNEASYPLEMCSHFDADEIKRLGKRFKGLDLDNSGSLSVVEFMSPLELQNPVLQVRVID 60
 Db |||||
 QY 1 MGNEASYPLEMCSHFDADEIKRLGKRFKGLDLDNSGSLSVVEFMSPLELQNPVLQVRVID 60
 Db |||||
 QY 61 IFDTDNGEVDPFKEFIEGVQSFSVKGDKLRFAPRIYDMDKGYISNGELFQVLKQMV 120
 Db |||||
 QY 61 IFDTDNGEVDPFKEFIEGVQSFSVKGDKLRFAPRIYDMDKGYISNGELFQVLKQMV 120
 Db |||||
 QY 121 GNNLKDTQLQOI VDKTIINADKDGRI SPFEFCVAVGGLDIHKQMVVDV 170
 Db |||||
 QY 121 GNNLKDTQLQOI VDKTIINADKDGRI SPFEFCVAVGGLDIHKQMVVDV 170
 Db |||||

RESULT 11
Q86YQ0

ID Q86YQ0 PRELIMINARY; PRT; 765 AA.
 AC Q86YQ0;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

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DE HGJ.
GN Name=H2GJ;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhou G., Yu L.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 4 WD repeats.
DR EMBL; AY183476; AA023957.1; -.
DR HSP; P41208; IM39.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR InterPro; IPR002048; EF-Hand.
DR InterPro; IPR010983; EF-Hand_Like.
DR InterPro; IPR008080; PARVALBUMIN.
DR InterPro; IPR001412; CRNA-synt_1.
DR InterPro; IPR001680; WD40.
DR InterPro; IPR011046; WD40_Like.
DR Pfam; PF00036; eFhnd; 4.
DR Pfam; PF00400; WD40; 4.
DR PRINTS; PR00320; GPOTINBRPT.
DR PRINTS; PR01697; PARVALBUMIN.
DR ProDom; PD000012; EF-hand; 2.
DR SMART; SM00054; EFh; 4.
DR SMART; SM00320; WD40; 4.
DR PROSITE; PS00178; AA_TRNA_LIGASE_I; UNKNOWN_1.
DR PROSITE; PS00018; EF_HAND; 4.
DR PROSITE; PS00082; WD_REPEATS_2; 1.
DR PROSITE; PS02094; WD_REPEATS_REGION; 1.
KW Calcium; Calcium-binding; Repeat; WD repeat.
SQ SEQUENCE 765 AA; 84720 MW; 6DC3CF99AB9C1F94 CRC64;

Query Match          90.9%; Score 795; DB 2; Length 765;
Best Local Similarity 100.0%; Pred.No. 4.9e-46;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GNEASYPLEMCSHPDADDEIKRLGRFKKLDLNSGSLSVVEFMSLPELQONPLVQRVIDI 61
DQ 65 GNEASYPLEMCSHPDADDEIKRLGRFKKLDLNSGSLSVVEFMSLPELQONPLVQRVIDI 124
QY 62 FDTDNGEVDVFKEFIEGVSVKGDKEQKLRFAFRYDMDKDGVIYNGELFQVLKMWVG 121
DQ 125 FDTDNGEVDVFKEFIEGVSVKGDKEQKLRFAFRYDMDKDGVIYNGELFQVLKMWVG 184

QY 122 NNLKDTLQQLQIVDKTIINADKDGGRISFEFCA 155
DQ 185 NNLKDTLQQLQIVDKTIINADKDGGRISFEFCA 218

RESULT 12
CALC DROME          STANDARD;          PRT;          170 AA.
AC Q24214; Q9V315;
DT 01-NOV-1997 (Rel. 35, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE 25-JAN-2005 (Rel. 46, Last annotation update)
DE Calcineurin B subunit, isoform 2 (Protein phosphatase 2B regulatory subunit).
DE subunit).
GN Name=CanB2; Synonyms=CNB2; ORFNames=CG11217;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Canton-S;
RX MEDLINE=97080513; PubMed=8921860; DOI=10.1016/0378-1119(96)00291-0;
RA Warren W.D., Phillips A.M., Howells A.J.;
RT "Drosophila melanogaster contains both X-linked and autosomal homologues of the gene encoding calcineurin B.";

```

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RL Gene 177:149-153 (1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RX MEDLINE=20196006; PubMed=107311132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Anantides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazek R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abail J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Baau A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Folsler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mout S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195 (2000).
RN [3]
RP GENOME REANNOTATION.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., M.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a systematic review.";
RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22 (2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley; TISSUE=Embryo, and Head;
RX MEDLINE=22426066; PubMed=12537569;
RA Stapleton M., Carlson J.W., Brokstein P., Yu C., Champe M.,
RA George R.A., Guarin H., Krommiller B., Pacleb J.M., Park S., Wan K.H.,
RA Rubin G.M., Celniker S.E.;
RT "A Drosophila full-length cDNA resource.";
RL Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8 (2002).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley; TISSUE=Embryo;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.W., E.,
RA Champe M., Chavez C., Dorsett V., Drensek D., Farfan D., Frise E.,
RA George R.A., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nunoo J., Pacleb J.M., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K.H., Yu C., Lewis S.E., Rubin G.M.,

```

RA Celniker S.E.;
 RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Calcineurin is a calcium binding and calmodulin binding
 CC protein found in all cells from yeast to mammals, it is a calcium
 CC dependent, calmodulin stimulated protein phosphatase (By
 CC similarity).
 CC -!- SUBUNIT: Composed of a catalytic subunit (A) and a regulatory
 CC subunit (B) (By similarity).
 CC -!- MISCELLANEOUS: This protein has four functional calcium-binding
 CC sites.
 CC -!- SIMILARITY: Contains 4 EF-hand calcium-binding domains.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
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 CC or send an email to license@isb-sib.ch).
 CC
 DR EMBL; U56245; AAC47350.1; -;
 DR EMBL; AE003840; AAF59195.2; -;
 DR EMBL; AY070642; AAL48113.1; -;
 DR EMBL; AY089602; AAL90340.1; -;
 DR EMBL; BT003768; AAO41447.1; -;
 DR PIR; JC5174; JCS174.
 DR HSSP; P06705; 1M63.
 DR FLYBase; FBGN0015614; CanB2.
 DR GO; GO:0008021; C:synaptic vesicle; NAS.
 DR GO; GO:0007269; P:neurotransmitter secretion; NAS.
 DR GO; GO:0016083; P:synaptic vesicle fusion; NAS.
 DR InterPro; IPR002048; EF-hand.
 DR InterPro; IPR010983; EF_Hand_Like.
 DR InterPro; IPR008080; Parvalbumin.
 DR InterPro; IPR001125; Recoverin.
 DR Pfam; PF00036; ehand; 4.
 DR PRINTS; PR01697; PARVALBUMIN.
 DR PRODOM; PD000450; RECOVERIN.
 DR SMART; SM00054; EFh; 4.
 DR PROSITE; PS00018; EF_HAND; 4.
 DR Calcium-binding; Repeat.
 FT CA_BIND 31 42 EF-hand 1 (Potential).
 FT CA_BIND 63 74 EF-hand 2 (Potential).
 FT CA_BIND 100 111 EF-hand 3 (Potential).
 FT CA_BIND 141 152 EF-hand 4 (Potential).
 FT CONFLICT 10 10 E -> D (in Ref. 4; AAL48113).
 FT CONFLICT 40 40 V -> I (in Ref. 4; AAL48113).
 FT CONFLICT 85 85 K -> R (in Ref. 4; AAL48113).
 FT CONFLICT 138 138 G -> C (in Ref. 4; AAL48113).
 SQ SEQUENCE 170 AA; 19267 MW; FDB1BD9DB5A4BDEC CRC64;
 Query Match 88.1%; Score 771; DB 1; Length 170;
 Best Local Similarity 87.6%; Pred. No. 4.6e-45;
 Matches 149; Conservative 10; Mismatches 11; Indels 0; Gaps 0;
 Qy 1 MGNREASYPLEMCSHFDADEIKRLGKRFKKLLDLSGSLSVSEEFMSLPQLQNPVQVRVID 60
 Db 1 MGNETSLPMECLSNFDFDADEIRRLGKRFKKLLDLSGSLSVSEEFMSLPQLQNPVQVRVID 60
 Qy 61 IFDFTDNGEVDPFKEFIEGVQSQFSVKGDKEQKLRFAFRFYDMDKGYISNGELFQVLKMWV 120
 Db 61 IFDADNGEVDPFKEFIEGVQSQFSVKGDKSLKLRFAFRFYDMDNDGYISNGELFQVLKMWV 120
 Qy 121 GNNLKDTQLQIQIVDKTIINADKDGGRISFEEFCFCAVVGGLDIHKQWVDV 170
 Db 121 GNNLKDTQLQIQIVDKTIINADKDGGRISFEEFCFCAVVGGLDIHKQWVDV 170
 RESULT 13
 Q7PQ91 PRELIMINARY; PRT; 169 AA.
 ID Q7PQ91
 AC Q7PQ91;

DT 01-MAR-2004 (TrEMBLrel. 26, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE ENSANGP00000013463 (ENSANGP00000024230) (Fragment).
 GN Name=ENSANGG00000010974; PEST.
 OS Anopheles gambiae str. PEST.
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anophelinae.
 OX NCBI_TaxID=180454;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PEST;
 RA Anopheles Genome Sequencing Consortium;
 RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AAA0100898; EAA09157.2; -;
 DR HSSP; P09860; 1DTL.
 DR GO; GO:0005509; F:calcium ion binding; IEA.
 DR InterPro; IPR02048; EF-Hand.
 DR InterPro; IPR010983; EF_Hand_Like.
 DR InterPro; IPR008080; Parvalbumin.
 DR InterPro; IPR001125; Recoverin.
 DR Pfam; PF00036; ehand; 4.
 DR PRINTS; PR01697; PARVALBUMIN.
 DR PRODOM; PD000450; RECOVERIN.
 DR PROSITE; PS00018; EF_HAND; 2.
 DR PROSITE; PS00018; EF_HAND; UNKNOWN_4.
 FT NON TER 1
 FT NON TER 1
 SQ SEQUENCE 169 AA; 19118 MW; DSD18F14C191601B CRC64;
 Query Match 87.9%; Score 769; DB 2; Length 169;
 Best Local Similarity 86.4%; Pred. No. 6.2e-45;
 Matches 146; Conservative 13; Mismatches 10; Indels 0; Gaps 0;
 Qy 2 GNEASYPLEMCSHFDADEIKRLGKRFKKLLDLSGSLSVSEEFMSLPQLQNPVQVRVID 61
 Db 1 GNETSLPMECLSNFDFDADEIRRLGKRFKKLLDLSGSLSVSEEFMSLPQLQNPVQVRVID 60
 Qy 62 FDTDNGEVDPFKEFIEGVQSQFSVKGDKEQKLRFAFRFYDMDKGYISNGELFQVLKMWV 121
 Db 61 FDADNGEVDPFKEFIEGVQSQFSVKGDKSLKLRFAFRFYDMDNDGYISNGELFQVLKMWV 120
 Qy 122 NNLKDTQLQIQIVDKTIINADKDGGRISFEEFCFCAVVGGLDIHKQWVDV 170
 Db 121 NNLKDTQLQIQIVDKTIINADKDGGRISFEEFCFCAVVGGLDIHKQWVDV 169
 RESULT 14
 CALB DROME STANDARD; PRT; 170 AA.
 ID CALB DROME STANDARD; PRT; 170 AA.
 AC P48451; Q9W4D0;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 25-JAN-2005 (Rel. 46, Last annotation update)
 DE Calcineurin B subunit, isoform 1 (Protein phosphatase 2B regulatory subunit).
 GN Name=canb; Synonym=CANB1, CNB, CNB1; ORFNames=CG4209;
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93054551; PubMed=1331060;
 RA Guerini D., Montell C., Klee C.B.;
 RT "Molecular cloning and characterization of the genes encoding the two
 RL subunits of Drosophila melanogaster calcineurin."
 RL J. Biol. Chem. 267:22542-22549 (1992).
 RN [2]
 RP SEQUENCE FROM N.A.

DR PRINTS; PRO0450; RECOVERIN.
DR SMART; SMO0054; EFH; 4.
DR PROSITE; PS00018; EF HAND; UNKNOWN 4.
SQ SEQUENCE 170 AA; 19357 MW; 5EC015B820097130 CRC64;
Query Match 87.7%; Score 767; DB 2; Length 170;
Best Local Similarity 86.5%; Pred. No. 8.6e-45;
Matches 147; Conservative 12; Mismatches 11; Indels 0; Gaps 0;
Qy 1 MGNASYPLEMCSHFDADIEIKRLGKRPKKLDLDNSGSLSVEEFMSLPQLQONPLVQRVID 60
Db 1 MGNENSLPWELCSNFDADIEIRLGRFKRLDLDNSGALSIDEFMSLPQLQONPLVQRVID 60
Qy 61 IFDTDGNGEVDFKEFIEGVQSQFSVKGDKQLRFAFRIYDMDKGYISNGELFQVLKMMV 120
Db 61 IFDADGNGEVDFKEFIOGVQSQFSVKGDKLSKLRFAFRIYDMNDGFIENGELFQVLKMMV 120
Qy 121 GNNLKDTQLQOIIVDKTIINADKDGGRISFEEFCVVGGLDIHKMMVVDV 170
Db 121 GNNLKDTQLQOIIVDKTILFADKDEGKISFEEFCVVGNTDIHKMMVVDV 170

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Job time : 60.073 secs

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